

(A) NAME/KEY: other  
(B) LOCATION: 20..65  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..47  
id W87295  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 327..368  
id W87295  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..312  
id AA248429  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 313..354  
id AA248429  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 76..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..269  
id W01758  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 270..311  
id W01758  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 30..201  
id AA249697  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..65  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..33  
                           id AA249697  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 257..289  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 222..254  
                           id AA249697  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 227..256  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 193..222  
                           id AA249697  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 19..180  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.3  
                           seq LIVWLLVKSFSSES/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

ATCTGGCTCA GTTCCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC	51
Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg	
-50 -45	
AGG TCT CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA TAT	99
Arg Ser Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr	
-40 -35 -30	
TCG GTG CTT TTA CCT ACC TAC AAC GAG CGC GAG AAC CTG CCG CTC ATC	147
Ser Val Leu Leu Pro Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile	
-25 -20 -15	
GTG TGG CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA	195
Val Trp Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu	
-10 -5 1 5	
ATT ATA ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT	243
Ile Ile Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala	
10 15 20	
GAA CAG TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA	291
Glu Gln Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro	
25 30 35	

CGA GAG AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CDY SRA ATG AAA 339  
Arg Glu Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys  
40 45 50

CAT GCA CAG GAA ACT ACA TCA TTA TTA TGG ATS CTG ATC TCT CAC 384  
His Ala Gln Glu Thr Thr Ser Leu Leu Trp Xaa Leu Ile Ser His  
55 60 65

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..268
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 13..245  
id AA134651  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 244..281  
id AA134651  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..353  
id W26888  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 7..208  
id T66207  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 263..325-  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 208..270  
                           id T66207  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 39..267  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..229  
                           id W00383  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 35..304  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 13..282  
                           id HSC36A071  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 207..266  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.3  
                           seq LLDSSLMASGTAS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AAACCGGGK TAGACGTACC TCACGGAAGC CGGCTTTGGC CCTGCGGCTK YTACCGTCGC      60
CGCGGAGAAA TTGTGGATC TGGCAGTCTA GGAATGAATC TCCTCTCAGC CTTTAAGCTC     120
ACCTGGTCAG AATCCTTGGA TGAGCCTGTG GGACCGTTCC TCCTAGCCCG GTGGTTTGGA     180
ACCA GTGGCT TTGGGACTGT AAGAGG ATG GAC AAA GAT TCT CAG GGG CTG CTA      233
          Met Asp Lys Asp Ser Gln Gly Leu Leu
          -20                      -15

GAT TCA TCC CTG ATG GCA TCA GGC ACT GCC AGC CGC TCA GAG GAT GAG      281
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu
-10                      -5                      1                      5

GAG TCA CTG GCA GGG CAG AAG CGA GCC TCC TCC CAG GCC CTG GGC ACC      329
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr
          10                      15                      20

GGG
Gly
332

```

## (2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 126..226  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                                   region 38..138  
                                   id AA009514  
                                   est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 252..343  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                                   region 161..252  
                                   id AA009514  
                                   est
- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 102..131  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                                   region 15..44  
                                   id AA009514  
                                   est
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 100..207  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
                                   seq CLAVSWEAAGCHG/AG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AAAGGAATAC TGACAGATAA GGCCGGAAAC AAAACTGATG GCTTGAAAAA CATTTTATG      60
GAATGTATTT ACTATCATTT TGTTTTACTA TAGAGGTAG ATG GGA CTC TTA ACT      114
                                     Met Gly Leu Leu Thr
                                     -35

TTT GGG TAC ATT GAA AMC AKG CKG AAA ACT GAA CAC AAT CCT GAT CAT      162
Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu His Asn Pro Asp His
-30                      -25                      -20

```

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 12..59  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: - score 4.1  
 seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGCGCGGGAA C ATG GGG CTG TAC GCT GCG GTG GCA GGC GTG CTG GCC GGC      50
      Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly
      -15                      -10                      -5

GTG GAG AGC CGC CAG GGC TCT AAT CAA GGG GCT GGT GTA CTC CAG CAA      98
Val Glu Ser Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln
      1                      5                      10

CTT CCA GAA CGT GAA RCA GCT GTA CGC GCT GGT GTG CGA AAS GCA GCG      146
Leu Pro Glu Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala
      15                      20                      25

CTA CTC CGC CGT GCT GGA TRC CGT GAT CTC CAR CGC CGG CCT CCT CAG      194
Leu Leu Arg Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln
      30                      35                      40                      45

TGC GAA GAA GCT
Cys Glu Glu Ala
                                         206
  
```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 299 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Heart

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 26..219  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 1..194  
                           id T06781  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 204..234  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 176..206  
                           id T06781  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 22..74  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 1..53  
                           id AA101354  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 71..110  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 51..90  
                           id AA101354  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 18..203  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
                           seq LDAVIASAGLLRA/EK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AAPAGGCGCG CGGGAAC ATG GGG CTG TAT GCT GCA GCT GCA GGC GTG TTG      50
      Met Gly Leu Tyr Ala Ala Ala Gly Val Leu
                -60                      -55

GCC GGC GTG GAG AGC CGC CAG GGC TCT ATC AAG GGG TTG GTG TAC TCC      98
Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser
-50                      -45                      -40

AGC AAC TTC CAG AAC GTG AAG CAG CTG TAC GCG CTG GTG TGC GAA ACG     146
Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr
-35                      -30                      -25                      -20

CAG CGC TAC TCC GCC GTG CTG GAT GCT GTG ATC GCC AGC GCC GGC CTC     194
Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu
                -15                      -10                      -5

CTC CGT GCG GAG AAG AAG CTG CGG CCG CAC CTG GCC AAG GTG CTA GTG     242
Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys Val Leu Val
                1                      5                      10

TAT GAG TTG TTG TTG GGA AAG GGC TTT CGA GGG GGT GGG GGC CGA TGG     290
Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp
    15                      20                      25

AAG GCC CGG                                                                299
Lys Ala Arg
    30

```

## (2) INFORMATION FOR SEQ ID NO: 292:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..458
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..163  
id R50658  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(413..458)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 442..487  
id AA016001  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 5..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

AGAA ATG GGT GCT CAG CAC ACA GCA CTT CTT CTA AAT ACA GAG GTG AGG	49
Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg	
-60 -55 -50	
TGG CTT TCT CGA GGT AAA GTT CTT GTA AGA CTT TTT GAA CTT CGT CGT	97
Trp Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg	
-45 -40 -35	
GAA CTT TTG GTT TTC ATG GAT TCT GCT TTT CGA CTA TCT GAT TGT TTA	145
Glu Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu	
-30 -25 -20	
ACA AAT TCA TCT TGG CTG CTA AGA CTT GCA TAT CTT GCA GAT ATT TTT	193
Thr Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe	
-15 -10 -5	
ACT AAA TTA AAT GAA GTT AAT TTG TCA ATG CAA GGA AAA AAT GTG ACC	241
Thr Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr	
1 5 10 15	
GTT TTT ACA GTA TTT GAT AAA ATG TCG TCA TTG TTA AGA AAA TTG GAA	239

Val	Phe	Thr	Val	Phe	Asp	Lys	Met	Ser	Ser	Leu	Leu	Arg	Lys	Leu	Glu	
				20					25					30		
TTT	TGG	GCC	TCA	TCT	GTA	GAA	GAA	GAA	AAC	TTT	GAT	TGT	TTT	CCT	ACA	337
Phe	Trp	Ala	Ser	Ser	Val	Glu	Glu	Glu	Asn	Phe	Asp	Cys	Phe	Pro	Thr	
			35					40					45			
CTC	AGT	GAT	TTT	TTG	ACT	GAA	ATT	AAT	TCT	ACA	GTT	GAT	AAA	GAT	ATT	385
Leu	Ser	Asp	Phe	Leu	Thr	Glu	Ile	Asn	Ser	Thr	Val	Asp	Lys	Asp	Ile	
		50					55					60				
TGC	AGT	GCC	ATT	GTG	CAG	CAC	CTA	AGG	GGT	TTG	CGC	GCT	ACT	CTG	TTA	433
Cys	Ser	Ala	Ile	Val	Gln	His	Leu	Arg	Gly	Leu	Arg	Ala	Thr	Leu	Leu	
	65				70					75						
AAA	TAC	TTT	CCT	GTA	ACA	AAT	GAC									457
Lys	Tyr	Phe	Pro	Val	Thr	Asn	Asp									
80					85											

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 19..206  
id AA044042  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..183  
id AA127902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..160  
id AA056679  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(99..247)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 302..450  
id W93399  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 11..158  
id R29154  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 117..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LVVMVPLVGLIHL/GW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

AATCCGCGGC AGAGCGGCTG CTTGAGATCT GTTTCTGGGG CCTCTGGCGG TGGCGGCCTG      60
TGGCGGCCTG GGGCGGCGCG ACGGCTGGTG CGCAGGTACA CTGATGCTGA AGTACT ATG      119
                                     Met
                                     -25

AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT GTT ATG GTC      167
Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met Val
          -20                      -15                      -10

CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC AGC      215
Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser Ser
          -5                      1                      5

CCT GTT TTC CAA ATA CCT AAA AAC GAC AAC ATG      248
Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
    10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 245..374  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 20..149  
                           id T41381  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 75..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```

AAAAATAAAA TGTAGGCAGC AAAAGTGGAA GAGGAGAGGC AGCTGGTGCA CTAATCCAGG      60
TCAGCAATCT GAAG  ATG  GTC  TTA  CGG  AGC  CTA  GTA  GAG  TAC  TCC  CAG  GAT      110
              Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp
              -50                      -45                      -40

GTC  CTG  GCG  CAT  CCT  GTG  TCA  GAA  GAG  CAT  CTC  CCA  GAT  GTG  AGC  CTC      158
Val Leu Ala His  Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu
              -35                      -30                      -25

ATT  GGA  GAG  TTC  TCA  GAC  CCG  GCA  GAG  CTC  GGC  AAG  CTG  CTT  CAG  CTG      206
Ile Gly Glu Phe  Ser Asp  Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu
              -20                      -15                      -10

GTG  CTG  GGC  TGT  GCC  ATC  AGT  TGC  GAG  AAA  AAG  CAG  GAC  CAC  ATC  CAG      254
Val Leu Gly Cys Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln
              -5                      1                      5

AGA  ATC  ATG  ACG  CTG  GAA  GAA  TCG  GTT  CAG  CAT  GTG  GTG  ATG  GAA  GCC      302
Arg Ile Met Thr Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala
              10                      15                      20                      25

ATC  CAA  GAG  CTC  ATG  ACC  AAA  GAC  ACT  CCT  GAC  TCC  CTG  TCA  CCA  GAG      350
Ile Gln Glu Leu Met Thr Lys Asp Thr  Pro Asp Ser Leu Ser Pro Glu
              30                      35                      40

ACG  TAT  GGC  AAC  TTT  GAC  AGC  CAG  TCC  CGC  AGT  ACT  GGG
Thr Tyr Gly Asn Phe Asp Ser Gln Ser Arg Ser Thr Gly
              45                      50

```

(2) INFORMATION FOR SEQ ID NO: 295:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 105..270  
id AA084830  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 64..93  
id AA084830  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 66..231  
id W01570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 26..55  
id W01570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..111  
id H82170  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 298..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 7..115  
id N71014  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 238..292  
id N35296  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 358..396
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MIHGFLAPTSA/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```
ATGGGGGCGG ASTAGCCGGA GCCGCGAGTC CATTTTGGGG CTGTGCTTGG CGCGTACCGT    60
GCGGTCCCTG TAGTTGGAGG ACGGGCGGTC GCGCSGGCCT TTCCCACTAG CCGGAGGTCTG   120
GAGATAAGTA CCCGCCGCCC GGCTTCTCTC GGGAAAGCGG GGTGGTCCTC GAACCTTCAG   180
CGAGGGTGGG GAGTTGCCCA GTAGCCTCTA GTTCGTTAGT CAAAACGTGA AAAAAAAGA   240
CCTGCTTTGC CVTGGGAAAT AGTAACCCTG CCAAATACAT CAGCTTGTAG GAGACAGAGG   300
ATGTGATGGA GCTGCTTGAA GAAGATCTCA CATGCCCTAT TTGTTGTAGT CTGTTTG    357
ATG ATC CAC GGG TTT TGC CTT GCT CCC ACA ACT TCT GCA AAA AAT GCT    405
Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
      -10                      -5                      1
```

## (2) INFORMATION FOR SEQ ID NO: 296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..86
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..63  
id C16698  
est

(A) NAME/KEY: other  
(B) LOCATION: 25..86  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 9..70  
id H48377  
est

[illegible][illegible][illegible]

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 90..140  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq RTWCLACVEASPG/QP

AAGCCTGGGA	CACCGCCGGC	GGGGAGAGAA	GCGGATCCCC	TCCGAGCCCC	GGCCCCAAGT		60
AACGCCGCCG	CCCCGGAGCC	GCCGTGAGT	ATG	CYT	TGT	CCC AGG ACC TGG TGT	113
			Met	Xaa	Cys	Pro Arg Thr Trp Cys	
					-15		-10
CTC GCC TGC GTT GAA GCA TCT CCA GGG CAG CCC TTC CTC CCG CCC CGC							161
Leu Ala Cys Val Glu Ala Ser Pro Gly Gln Pro Phe Leu Pro Pro Arg							
	-5				1		5
CCC GGG							167
Pro Gly							

## (2) INFORMATION FOR SEQ ID NO: 297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 93..226  
id W81645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 31..95  
id W81645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 62..195  
id W06951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..64  
id W06951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..179  
id W38711  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide



- (B) LOCATION: 24..86  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

GCNGTCGGCT CCGCGGCGCC GCC ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC   53
                        Met Ala Asp Val Glu Asp Gly Glu Glu Thr
                        -20                               -15

TGC GCC CTG GCC TCT CAC TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC   101
Cys Ala Leu Ala Ser His Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly
-10                               -5                               1                               5

GAC AAG ATG TTC TCC CTC AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC   149
Asp Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser
                        10                               15                               20

TGG GAC GTG GAG TGC GAT ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG   197
Trp Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met
                        25                               30                               35

GAT GCC TGT MTT AGA TGT CAA GCG GGG                               224
Asp Ala Cys Xaa Arg Cys Gln Ala Gly
                        40                               45
  
```

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: 122..188  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 198..264  
 id R58050  
 est

(ix) FEATURE:

- (A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 193..259  
 id H98670

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 194..260  
                           id N66980  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 198..264  
                           id AA159781  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(122..188)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 161..227  
                           id H45410  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 273..350  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
                           seq IIMFLLIIVCGSP/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

TAGAAGTAGC AGGATCGCCT TAATAATAAT AATAGTTTGT TAGCATGAAG CCTGAGCATT   60
GTCCAAAGTT TGGAAATGTG AACGCTGATA GTCACATCTG TCCATCTTTC CACATTTCTA  120
GGATGCTGAC AGACAGCACC AAGAAGTAAT TGCAATTTAT CGGACACACC TTCTTAGTGC  180
TGCACAGGTA AAGAACTACT TCTCCTTTGG AAAGAATATT GCTTTAGAGA TAATAATTTT  240
TATTTTCAAA TAAATTTATG TGAAAGTAAT TG ATG TTT AAA GTA GCT GCA CCC   293
                               Met Phe Lys Val Ala Ala Pro
                               -25                               -20

CCT ATG CTT ATT TAA KAA ATA ATT ATG TTT CTT TTA ATC ATT GTT TGT   341
Pro Met Leu Ile Xaa Xaa Ile Ile Met Phe Leu Leu Ile Ile Val Cys
          -15                               -10                               -5

GGA TCT CCC AGG CCG                                           356
Gly Ser Pro Arg Pro

```

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 228..322  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..46)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 363..408  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 315..364  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 67..161  
id T32629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 154..246  
id T32629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(87..181)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 230..324  
id W61289  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(6..93)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 317..404  
id W61289  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(87..181)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 232..326  
id N53422  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(3..93)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 319..409  
id N53422  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..181  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 78..172  
id N50275  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..85  
id N50275  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 64..126  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXMCLWSLRNLF/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AGCTATTTGG ATAGTGTAGC TTAAATGTGC TGCACATGAT ACTGGCAGCC CTAGAGTTCA    60
TAG ATG GAC TTT TGG GAC CCA GCA GTT TTT RAA ATG TGT TTA TGG AGT    108
  Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser
    -20                      -15                      -10

TTA AGA AAT TTA TTT TCC AGG TGC AGC CCC TGT CTA ACT GAA ATT TCT    156
Leu Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser
    -5                      1                      5                      10

CTT CAC CTT GTA CAC TTG ACA GCT GAA AAA AAA CAA CAT GGG AGT AAT    204
Leu His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn
          15                      20                      25

AAT GGG TCG GCG
Asn Gly Ser Ala
          30

```

## (2) INFORMATION FOR SEQ ID NO: 300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..114  
id R56502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 162..258  
id R56502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 119..162  
id R56502

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 160..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq SVPLLSLSHSIGI/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```
AGTGACCAAA TGA CTTAACC ACAGATGGAG TGAAGACAGG GGTA ACTGCT TGGTCTGGTC    60
CCCAGTAGAG CATTGCTCAC TATAAACCAC AAGCTGCTTC TAATTTATTT GAGRTGKTAW    120
TAAYCGTGGS CCTTKATATT CTGGTCTCTC TTGCTGCAA ATG AGT CCG GCA GGC        174
                               Met Ser Pro Ala Gly
                               -30

AAG CAC AAC TCA GAA AGC AAA TTC ACC TTC TTT GTA GCC CTT GAT GGG        222
Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe Val Ala Leu Asp Gly
                               -25                -20                -15

TCG GTC CCC CTG TTG TCT CTT TCT CAT TCC ATA GGC ATT TCC CCC ACA        270
Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile Gly Ile Ser Pro Thr
                               -10                -5                1

AGG                                                                273
Arg
```

## (2) INFORMATION FOR SEQ ID NO: 301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 149..231  
id H15081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..71)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 238..308  
id H15081  
- est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..71)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 234..303  
id H16744  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 148..230  
id R61691  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..72)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 236..306  
id R61691  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..85)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 223..306  
id H17833  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(109..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 148..199  
id H17833  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 23..73
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LVCVGLHTEGPWG/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

ATGTGGTGBT TGTGTCTTAA CT ATG CAC TGG GCC CTT GTC TGC GTC GGC TTG  
Met His Trp Ala Leu Val Cys Val Gly Leu

-15

-10

CAT	ACA	GAG	GGC	CCC	TGG	GGT	CGG	CCC	TCC	GGC	CTG	GCC	TCA	GCC	AGT	100
His	Thr	Glu	Gly	Pro	Trp	Gly	Arg	Pro	Ser	Gly	Leu	Ala	Ser	Ala	Ser	
		-5					1					5				
GGG	ATG	GAC	AGG	GCC	AGG	CAG	GCC	TCT	GAA	CTT	CCA	CCT	CCT	GGG	GCC	148
Gly	Met	Asp	Arg	Ala	Arg	Gln	Ala	Ser	Glu	Leu	Pro	Pro	Pro	Gly	Ala	
10					15					20					25	
TCC	CAG	ACC	CCC	CAG												163
Ser	Gln	Thr	Pro	Gln												
				30												

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 155..325  
id H16532  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..58  
id H16532  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 170..340  
id H17763  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..62



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..55  
id H17763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 168..247  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 11..62  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..52  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 183..222  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 268..307  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 111..263  
id AA084554  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..256  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 136..306  
id R52491  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 20..235  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AGAGCTCGCT GTGGCCCGG ATG TTC GGT GCA GCT GCC AGA TCC GCT GAT CTA	52
Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu	
-70 -65	
GTG CTT CTC GAA AAA AAC CTT CAG GCG GCC CAT GGG TAT GCC CAA GAG	100
Val Leu Leu Glu Lys Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu	
-60 -55 -50	
GAC AGA GAA CGA ATG CAC AGA DRT ATT GTC AGC CTT GSA CAG AAT CTC	148
Asp Arg Glu Arg Met His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu	
-45 -40 -35 -30	
CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG CAA TGC TTC CTC	196
Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu	
-25 -20 -15	
TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG GGA AAA AGA GTT	244
Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val	
-10 -5 1	
CCA GCG CAC TTT	256
Pro Ala His Phe	
5	

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..114  
id N87112  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..81  
id AA094982  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..130

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
                          region 1..79  
                          id T68050  
                          est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
                          region 1..84  
                          id AA157180  
                          est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
                          region 1..81  
                          id AA186993  
                          est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 43..123  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
                          seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

AGCCGGAGCA AAGTTTCACT TATAGAAGGG AGAGGAGCGA AC ATG GCA GCG CGT	54
Met Ala Ala Arg	
-25	
TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC	102
Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val Ala Leu Leu Ile	
-20                          -15                          -10	
GTT TGC GAC GTT CCC TCA GCC TCT GCC CGG	132
Val Cys Asp Val Pro Ser Ala Ser Ala Arg	
-5  1	

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 73..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 16..181  
id W32979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 316..394  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 260..338  
id W32979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..322  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 194..265  
id W32979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..437  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 107..293  
id AA128556  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..94  
id AA128556  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..381  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 104..234  
id T20234  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98

```

region 6..91
id T20234
. est

```

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 383..437  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 235..289  
id T20234  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 115..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 65..188  
id T32594  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 201..268  
id T32594  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 52..115  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..64  
id T32594  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 245..292  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LLLQPSMIOEVWT/XY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

ATCAGACGCC	AGTATAAGCC	TTTGAGTCTC	AATAGACTGC	AGTATCTTAT	TGATTTGGGT	60		
CGTGTTGATC	CTAGTCAACC	TATTGACTTA	ACCCAGCTTG	TCAATGGGAG	AGGTGTGACC	120		
ATCCAGCCAC	TTAAAAGGGA	TTATGGTGTC	CAGCTGGTTG	AGGAGGGTGC	TGACACCTTT	180		
ACGGCAAAAG	TTAATATTGA	AGTACAGTTG	GCTTCAGAAC	TAGCTATTGC	TGCCATTGAA	240		
AAAA ATG	GTG GTG	TTG TTA	CTA CAG	CCT TCT	ATG ATC	CAA GAA	GTC TGG	289
	Met Val	Val Leu	Leu Leu	Gln Pro	Ser Met	Ile Gln	Glu Val	Trp
	-15		-10			-5		

ACA THG TAT GCA AAC CTG TTC CAT TCT TTC TTC GTG GAC AAC CCA TTC	337
Thr Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe	
1 5 10 15	
CAA AAA GAA TGC TTC CAC CAG AAG AAC TGG TAC CAT ATT ACA CTG ATG	385
Gln Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met	
20 25 30	
CAA AGA ACC GTG GGT ACC TGG CGG ATC CTG CCA AAT TTC CTG AAG CAC	433
Gln Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His	
35 40 45	
GAC	436
Asp	

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..407
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.5  
region 1..326  
id HSARSE  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..171
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..84  
id AA160312  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 149..241
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LAVLLSLAPSASS/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

AAAACTCGAA GTTAATCATT CCCAGCTCAA AGCCTTGTC AAGTGCTCTC TGCCTTCACG	60
CTTGCTTCCT TTGGGAGAGA ACCTTCCTCT TCTTGATCGG GGATTCAGGA AGGAGCCCAG	120
GRGCAGAGGA AGTAGAGAGA GAGRCAAC ATG TTA CAT CTG CAC CMT TCT TGT	172
Met Leu His Leu His Xaa Ser Cys	
-30 -25	
TTG TGT TTC AGG AGC TGG CTG CCA GCG ATG CTC GCT GTA CTG CTA AGT	220
Leu Cys Phe Arg Ser Trp Leu Pro Ala Met Leu Ala Val Leu Leu Ser	
-20 -15 -10	
TTG GCA CCA TCA GCT TCC AGC GAC ATT TCC GCC TCC CGA CCG AAC ATC	268
Leu Ala Pro Ser Ala Ser Ser Asp Ile Ser Ala Ser Arg Pro Asn Ile	
-5 1 5	
CTT CTT CTG ATG GCG GAC GAC CTT GGC ATT GGG GAC ATT GGC TGC TAT	316
Leu Leu Leu Met Ala Asp Asp Leu Gly Ile Gly Asp Ile Gly Cys Tyr	
10 15 20 25	
GGC AAC AAC ACC ATG AGG ACT CCG ARN ATT GAC CGC CTT GCA GAG GAC	364
Gly Asn Asn Thr Met Arg Thr Pro Xaa Ile Asp Arg Leu Ala Glu Asp	
30 35 40	
GGC GTG AAG CTG ACC CAA CAC ATC TCT GCC GCA TCT TTG TGC	406
Gly Val Lys Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys	
45 50 55	

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 15.8  
seq LLLLLLLLRHGAQG/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His  
-20 -15 -10 -5  
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala  
1 5

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14  
seq LAMLALLSPLSLA/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
-25                               -20               -15           -10

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa
                    -5                      1                5

Xaa Pro Glu Tyr Phe Gln Gln Pro
      10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.3  
seq HILFLLLLPVAAA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
      -15                      -10                -5

```



Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr  
1 5 10  
Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro  
15 20 25 30  
Leu Leu Ala Gly Leu Val Ala  
35

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.2  
seq LALALGLAQPASA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu  
-20 -15 -10  
Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu Leu  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.9

seq LVLEFLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser  
 -20                               -15                               -10                               -5

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu  
                                   1                               5                               10

Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val  
                   15                               20                               25

Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp Glu  
           30                               35                               40

Glu Glu Thr Thr Phe Arg Met Glu Ser Gly  
   45                               50

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3  
seq PLLSSLLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala  
 -15                               -10                               -5

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro  
   1                               5                               10                               15

Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro Thr  
                   20                               25                               30

Arg Leu Asp Arg Val Tyr Pro Ser Arg  
           35                               40

(2) INFORMATION FOR SEQ ID NO: 312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LWLLFFLVTAIHA/EL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu
      -10                      -5                      1
Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg
      5                      10                      15
Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr
      20                      25                      30
Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg
      35                      40                      45                      50
Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
      55                      60                      65
Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu
      70                      75                      80
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile
      85                      90                      95
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile
      100                     105                     110
Pro Ser Thr Leu Ala Pro Thr Arg
      115                     120

```

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LPLLCLFLQGATA/VL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg Arg Leu Gln Leu Pro  
-25 -20 -15

Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala Val Leu Phe Ala Val  
-10 -5 1 5

Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala Leu Trp Xaa Arg Lys  
10 15 20

Leu Gly

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq ALALLLVLP LLWP/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Lys Trp Pro Trp Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val  
-35 -30 -25

Leu Ser Pro Pro Cys Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Leu  
-20 -15 -10

Val Leu Pro Leu Leu Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys  
-5 1 5

Xaa Pro Ser Pro Ala Arg Arg

10

15

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq PLLGLLLSLPAGA/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu Leu
      -20                      -15                      -10
Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys Gly Glu
      -5                      1                      5
Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala Asp Ile Pro
      10                      15                      20                      25
Tyr Gln Glu Ile Ala Xaa Glu His Leu Arg Ile Cys Pro Gln Glu Tyr
      30                      35                      40
Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu Ser Gln Gln Ser Lys
      45                      50                      55
Leu Glu Phe Glu Asn Leu Val Glu Glu Thr Ser His Phe Val Arg Thr
      60                      65                      70
Thr Phe Val Ser Arg His Lys Lys Phe Asp Gly Arg
      75                      80                      85

```

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10  
seq LWLSLLVPSC/LCA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Leu Leu His Trp Val Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu  
                  -25                  -20                  -15

Trp Leu Ser Leu Leu Val Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro  
                  -10                  -5                  1

Leu Pro Ser Leu Pro Leu Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu  
  5                                  10                                  15                                  20

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -34..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.6  
seq LLLFSLVSPPTC/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala  
                  -30                  -25                  -20

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro  
                  -15                  -10                  -5

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala  
  1                                  5                                  10

Trp Xaa Thr Pro Pro Thr Arg Trp  
  15                                  20

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq AMWWLLWGVLQA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35                               -30               -25           -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
               -15                     -10           -5

Leu Gln Ala Trp Pro Xaa Pro Gly Leu Arg Pro Leu Gly Pro Arg Ala
              1                5                10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
   15                20                25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
   30                35                40                45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
              50                55                60

Gly Leu Xaa Xaa Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Val Leu
   65                70                75

Trp Ser Ala Arg Leu Pro Ser Gly Gln Ala Pro Trp Ser Glu Gly
   80                85                90

```

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -37..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq LLAVLLASWRLWA/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```

Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
  -35                      -30                      -25

Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
  -20                      -15                      -10

Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
  -5                      1                      5                      10

Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
      15                      20                      25

Ser Leu Ser Lys Ser Pro Gly
      30

```

## (2) INFORMATION FOR SEQ ID NO: 320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -55..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq SLLLLSTALNILA/CQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```

Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln Leu Gln Lys
-55                      -50                      -45                      -40

Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg Asn Ile Leu
      -35                      -30                      -25

Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu Leu Ser

```



-20                                  -15                                  -10  
Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu Leu Gly  
          -5  1  5

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu  
          -15                                  -10                                  -5  
Ser Cys Val Gln Ala Xaa Xaa  
          1  5

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LCLVCLLVHTAFR/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Gln Leu Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr  
                     -15                    -10                    -5

Ala Phe Arg Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp  
                     1                            5                            10

Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro  
           15                            20                            25

Glu Arg  
   30

## (2) INFORMATION FOR SEQ ID NO: 323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq ILLCSVAVXLSPS/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Cys Ile His Xaa Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala  
      -30                            -25                            -20

Leu Lys Ile Leu Leu Cys Ser Val Ala Val Xaa Leu Ser Pro Ser Glu  
      -15                            -10                            -5                            1

Pro Leu Ala Pro  
           5

## (2) INFORMATION FOR SEQ ID NO: 324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

```

Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys Ala Asn
   -35                               -30                       -25

Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser Leu Phe
   -20                               -15                       -10

Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg Tyr Arg
   -5                               1                         5                10

Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro Arg Ala
          15                               20                       25

Gly Thr Cys Arg Thr Pro Thr
          30

```

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq HLWILLLESFCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

```

Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu Thr Lys His Asp Phe
-30                               -25                       -20                       -15

Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe Cys Trp Met Ser Arg
          -10                               -5                1

Ser Phe Phe Phe Phe
          5

```

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLFFHILFHSCFS/HL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His  
-20 -15 -10 -5

Ser Cys Phe Ser His Leu Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLCSALAWQQSLS/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly Gly Val Lys Ile Tyr  
-65 -60 -55

Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala Met Met Asn Ser Ile

-50                      -45                      -40  
 Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu Leu Glu Ser Pro Thr  
     -35                      -30                      -25  
 Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser Ala Leu Ala Trp Gln  
     -20                      -15                      -10                      -5  
 Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly Val Ser Glu Lys Ala  
                             1                      5                      10  
 Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His Ser Lys Asp Phe Thr  
             15                      20                      25  
 Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His Phe Asn Tyr Pro Ser  
         30                      35                      40  
 Thr Pro Arg  
     45

## (2) INFORMATION FOR SEQ ID NO: 328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq FVRFLGFVSCLQS/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser Tyr Ser Leu Leu Phe  
             -25                      -20                      -15  
 Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln Ser Asp Pro Ile Cys  
         -10                      -5                      1  
 Ser Phe Phe Phe Phe  
     5

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8  
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser  
-20 -15 -10

Ser Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn  
-5 1 5

Pro Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu  
10 15 20

Ala Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro  
25 30 35 40

Val Gly Ile Asp Ser Gly Ser Leu  
45

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8  
seq IIPLIXXLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Gly Ser Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu

-20

-15

-10

Ser Leu Cys Leu Cys Leu Trp Trp Arg Ile Ile  
 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq VCLLCSCGSCAWS/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Leu Gln Val Ala Thr Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val  
 -30 -25 -20

Lys Pro Val Cys Leu Leu Cys Ser Gly Cys Ser Cys Ala Trp Ser Val  
 -15 -10 -5 1

Gly Cys Val Xaa Glu Ser Glu Ser Glu  
 5 10

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7

seq PFFLALCFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Phe Cys Leu Ala Pro Phe Phe Leu Ala Leu Cys Phe Pro Lys Ser  
                   -15                                  -10                                  -5

Thr Ser Gln Pro Gln Arg  
                   1

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
                                   seq QCLLCISPPVFC/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln  
                   -30                                  -25                                  -20

Leu Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys  
                   -15                                  -10                                  -5

Glu Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys  
                   1                                  5                                  10                                  15

Glu Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val  
                   20                                  25                                  30

Ser Pro Leu Ala Ala Trp Met Val  
                   35                                  40

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly
      -20                      -15                      -10
Leu Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His
      -5                      1                      5
Pro Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser
  10                      15                      20                      25
Asp Arg

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq FIXFPFLFPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Cys Leu Leu Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe
      -15                      -10                      -5
Ser Phe Ser Gln Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly
      1                      5                      10
Ser His Pro Glu Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys
  15                      20                      25

```

Ala Arg Pro Gln Pro Pro Leu Phe His Pro Phe Ile Ser Ser  
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLVASGXAEGVSA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Ala Ser Glu Arg Xaa Pro Asn Arg Pro Xaa Cys Leu Leu Val Ala  
 -25 -20 -15 -10

Ser Gly Xaa Ala Glu Gly Val Ser Ala Gln Ser Phe Leu Xaa Cys Phe  
 -5 1 5

Thr Met Ala Ser Thr Xaa Phe Asn Leu Gln Val Ala Xaa Pro Gly Gly  
 10 15 20

Lys Ala Met Glu Phe Val Asp Val Thr Xaa Ser Asn Ala Arg Trp Val  
 25 30 35

Gln Asp  
 40

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
 seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```

Met Phe Pro Asp Tyr Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln
-25                -20                -15                -10

Leu Val Phe Leu Arg Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg
                -5                1                5

His Leu His Asn Ile Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly
    10                15                20

Ser Cys Ile Gln Lys Gln Pro Gly
    25                30
  
```

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
 seq LLLXLXLLLIAlE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

```

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
-25                -20                -15                -10

Leu Xaa Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
                -5                1                5

Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
    10                15                20

Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
    25                30                35

Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
    40                45                50                55
  
```

Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu  
60 65 70

Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys  
75 80

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq TFLLLLFXNAGRS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Thr Phe Leu Leu Leu Leu Phe Xaa Asn Ala Gly Arg Ser Leu Arg  
-10 -5 1

Met Cys

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq EMFLVLLVTGVHS/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met Phe  
 -25 -20 -15

Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr Ala Lys  
 -10 -5 1 5

Lys Ile Lys Arg Pro Gly  
 10

## (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq ISLLFIFFSIANS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Ser Ser Pro Leu Leu Val Glu Gln Ser Ser Thr Lys Ser Pro Lys  
 -40 -35 -30 -25

Ser Trp Ser Trp Ser Phe Leu Ala Phe Ser Cys Ile Ser Leu Leu Phe  
 -20 -15 -10

Ile Phe Phe Ser Ile Ala Asn Ser Ser Pro Cys Gly  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq IPLLLFFHLSFL/NS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Tyr Leu Phe Cys Leu Phe Ser Val Ser Lys Thr Ile Pro Leu Leu  
 -25                      -20                      -15                      -10

Leu Leu Phe Phe His Leu Ser Phe Leu Asn Ser Leu  
                     -5                                      1

## (2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq CLLILKFLSPAET/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Ile Val Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr  
 -15                      -10                      -5

Ser Ile Leu Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val  
   1                      5                      10                      15

Pro Leu Glu Val Ser Gln Ile Leu Gln Thr Gln  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.7  
seq LILCFLFILHTHT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys  
-25 -20 -15 -10

Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His Thr His  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -36..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.7  
seq IFDLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Phe Phe Ile Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu  
-35 -30 -25

Ala Met Lys Pro Arg His Pro Ile Phe Asp Leu Leu Leu Leu Leu Xaa  
-20                      -15                      -10                      -5

Xaa Ser Asn Gln Leu Pro Val Thr Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LWPFLTWINPALS/IC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro  
-60 -55 -50 -45

Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro  
-40 -35 -30

Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu  
-25 -20 -15

Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro  
-10 -5 1

Leu Gly Ser Cys Gly Trp Gln  
5 10

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSALWFCHPCCL/CC



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Leu Gln Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys
  -15                      -10                      -5
Leu Cys Cys Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln
  1                      5                      10                      15
Gly Gly Ser Gly Cys Pro
                      20

```

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

Met Met Asp Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly
  -15                      -10                      -5
Pro His Gln Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn
  1                      5                      10
Leu Pro Lys Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp
  15                      20                      25
Lys Ala Glu Gln Glu Arg Val Glu Val Glu
  30                      35

```

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq LLPGLPLVRTSFS/HF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Met Pro Pro Cys Leu Leu Pro Gly Leu Pro Leu Val Arg Thr  
-15 -10 -5

Ser Phe Ser His Phe Phe Ser Leu Ser Gly Gly Thr Thr Thr Ala Arg  
1 5 10

Gly

## (2) INFORMATION FOR SEQ ID NO: 350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.5  
seq GLAMLHVTRGVXG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu Ala Met  
-25 -20 -15 -10

Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg Val Arg Val Xaa Xaa  
-5 1 5

Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala Leu Ser Ser Xaa Ala  
10 15 20

Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp  
25 30

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq LLILLCSSPPDRV/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile Leu Leu  
                   -20                                  -15  -10

Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val Leu His  
-5 1 5

Ser Leu Leu Gln Leu Pro Ala Gln  
10 15

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq FALLFLFLVPVPG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Arg Ile His Tyr Leu Leu Phe Ala Leu Leu Phe Leu Phe Leu Val  
-20 -15 -10 -5

Pro Val Pro Gly His Gly Gly Ile Ile Asn Thr Leu Gln Lys Tyr Xaa

1 5 10  
Leu Gln Ser Gln Arg Arg Pro Val Cys Cys Ala Gln Leu Pro Ser Lys  
15 20 25  
Gly Glu Arg  
30

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq MCLLTALVTQVIS/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys  
-10 -5 1  
Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro  
5 10 15  
Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro  
20 25 30 35  
Thr Val Tyr Ser Ser  
40

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq GLALVAGTPPSRS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly Thr Pro Pro Ser  
-15 -10 -5

Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq PCVSLWAPRXFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu Met  
-35 -30 -25

Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu Trp  
-20 -15 -10

Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr Leu  
-5 1 5 10

Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys Asp  
15 20 25

Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His Cys  
30 35 40

Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr  
45 50

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq SLLXLRASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu Leu Xaa Leu  
-20 -15 -10

Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa Xaa Cys Pro  
-5 1 5

Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr  
10 15

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- ```
{A} NAME/KEY: sig_peptide
{B} LOCATION: -81..-1
{C} IDENTIFICATION METHOD: Von Heijne matrix
{D} OTHER INFORMATION: score 6.3
                        seq FLSSLXSVSETPG/SL
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ala Gly Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro  
-30 -75 -70

Gly Arg Leu Ser Arg Ala Arg Ala Ser Val Val Arg Trp Ser Pro Arg  
 -65 -60 -55 -50  
 Ala Thr Ala Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln  
 -45 -40 -35  
 Glu Leu Val Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala  
 -30 -25 -20  
 Thr Ala Asp Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro  
 -15 -10 -5  
 Gly Ser Leu Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp  
 1 5 10 15  
 Gly Arg

## (2) INFORMATION FOR SEQ ID NO: 358:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LWCFFHSFISFSLSS/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Trp Xaa Gly Ser Leu Trp Cys Phe His Ser Phe Ile Ser Phe  
 -15 -10 -5  
 Ser Leu Ser Ser Ser Arg  
 1

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq FLLTFFSYSLLHA/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
  -35                      -30                      -25

Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
-20                      -15                      -10                      -5

Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
                      1                      5                      10

Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
          15                      20                      25

Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
  30                      35                      40

```

## (2) INFORMATION FOR SEQ ID NO: 360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq WILAVGLSLPSSS/XI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

```

Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val Gly Leu Ser Leu Pro
          -15                      -10                      -5

Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu Tyr Ser
          1                      5                      10

```



## (2) INFORMATION FOR SEQ ID NO: 361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LCGLLHLWLKVFS/LK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn  
-35                      -30                      -25                      -20

His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys  
                    -15                      -10                      -5

Val Phe Ser Leu Lys Gln Leu Lys Lys  
                    1                                      5

## (2) INFORMATION FOR SEQ ID NO: 362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LFLNLCILAXPFS/KQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```

Met Asn Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys
    -20                      -15                      -10

Ile Leu Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr
    -5                      1                      5

Val Ser Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile
    10                      15                      20                      25

Ser Ile Val Tyr Thr Leu
                30

```

## (2) INFORMATION FOR SEQ ID NO: 363:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq VVLAWGLLNVSMA/GM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Met Gln Gly Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr
-40                      -35                      -30                      -25

Ile Lys Met Arg Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp
    -20                      -15                      -10

Gly Leu Leu Asn Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr
    -5                      1                      5

Gly Lys Leu Ile Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp
    10                      15                      20

Tyr Xaa Glu Leu Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe
    25                      30                      35                      40

Asp Phe Trp Arg Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val
    45                      50                      55

Val Ser Pro Gly Arg
                60

```

## (2) INFORMATION FOR SEQ ID NO: 364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq PXXLLILAHITQS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Met Asn Gln Thr His Pro Xaa Xaa Leu Leu Ile Leu Ala His Ile  
                  -15                  -10                  -5

Thr Gln Ser Cys Pro Trp Ala His Val Gly Ala Ala Pro Ser Ala Leu  
                  1                          5                          10

Leu Ile His Arg Trp Glu Leu Arg Gly Cys Ser Tyr Leu Lys Leu Phe  
          15                          20                          25

Leu Val Met Val Leu Ile Phe Glu Met Leu  
          30                          35

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq GLVLLLSLAEILF/KI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Leu Pro Glu Arg Arg Gly Leu Val Leu Leu Leu Ser Leu Ala  
 -20 -15 -10 -5

Glu Ile Leu Phe Lys Ile Met Ile Leu Glu Gly Gly Gly Val Met Asn  
 1 5 10

Leu Asn Pro Gly Asn Asn Leu Leu His Gln Pro Pro Ala Trp Thr Asp  
 15 20 25

Ser Tyr Ser Thr Cys Asn Val Ser Ser Gly Phe Phe Gly Gly Gln Trp  
 30 35 40

His Glu Ile His Pro Gln Tyr Trp Thr Lys Tyr Gln Val Trp Glu Trp  
 45 50 55 60

Leu Gln His Leu Leu Asp Thr Asn Gln Leu Asp Ala Asn Cys Ile Pro  
 65 70 75

Phe Gln Glu Phe Asp Ile Asn Gly Glu Xaa Arg  
 80 85

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LCWALLYNCFSSS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro Leu  
 -25 -20 -15

Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro Val  
 -10 -5 1

Ala Leu Val  
 5

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ALLASLGIAFSRS/RA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg Arg Leu  
-85 -80 -75 -70

Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp Xaa Xaa  
-65 -60 -55

Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val Tyr Phe  
-50 -45 -40

Ser Arg Glu Glu Trp Glu Leu Leu Asp Asp Ala Gln Arg Leu Leu Tyr  
-35 -30 -25

His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu Gly Ile  
-20 -15 -10

Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7  
seq FLCFLNLTSHLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met  Leu  Ile  Thr  Arg  Leu  Gln  Ser  Gly  Ile  Asp  Phe  Ala  Ile  Gln  Leu
-55                                -50                                -45

Asp  Glu  Ser  Thr  Asp  Ile  Gly  Ser  Cys  Thr  Thr  Leu  Leu  Val  Tyr  Val
-40                                -35                                -30                                -25

Arg  Tyr  Ala  Trp  Gln  Asp  Asp  Phe  Leu  Glu  Asp  Phe  Leu  Cys  Phe  Leu
-20                                -15                                -10

Asn  Leu  Thr  Ser  His  Leu  Ser  Gly  Leu  Asp  Ile  Phe  Thr  Glu  Leu  Glu
-5                                1                                5

Arg  Arg  Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

```
(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -38..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 5.7
                               seq LAFLSCLAFLVLDTQ
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Pro | Gln | Leu | His | Cys | Ile | Leu | Asn | Ser | Asn | Ser | Val | Ala |
|     |     |     | -35 |     |     |     |     | -30 |     |     |     |     | -25 |     |     |
| Cys | Ser | Phe | Ala | Val | Gly | Ala | Gly | Phe | Leu | Ala | Phe | Leu | Ser | Cys | Leu |
|     |     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |     |     |     |
| Ala | Phe | Leu | Val | Leu | Asp | Thr | Gln | Glu | Thr | Arg | Ile | Ala | Gly | Thr | Arg |
|     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |
| Phe | Lys | Thr | Ala | Phe | Gln | Leu | Leu | Asp | Xaa | Ile | Leu | Ala | Val | Leu | Trp |
|     |     |     | 15  |     |     |     |     |     | 20  |     |     |     |     | 25  |     |

## (2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Muscle
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -28..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.7  
                                seq DHLFLLFPRSCSS/LV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn Thr Asp  
          -25                                -20                                -15

His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val  
          -10                                -5                                1

## (2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 26 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -24..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.6  
                                seq FFFFLFLLPPXP?/TG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Glu Leu Lys Gln Leu Gly Pro Arg Ser Phe Phe Phe Phe Leu  
          -20                                -15                                -10

Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly  
          -5                                1

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LILPALFFFPLHC/TF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr Ser Leu Ile Leu  
-25 -20 -15

Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe His Gly Leu Thr  
-10 -5 1 5

Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro Thr  
10 15

## (2) INFORMATION FOR SEQ ID NO: 373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LLLCMDLPHSVLS/NW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu Cys



-25                      -20                      -15                      -10  
Met Asp Leu Pro His Ser Val Leu Ser Asn Trp  
                         -5                                      1

## (2) INFORMATION FOR SEQ ID NO: 374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq EFLFLGFPSNSWP/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe Pro  
-20                                      -15                                      -10  
Ser Asn Ser Trp Pro His Arg  
-5                                      1

## (2) INFORMATION FOR SEQ ID NO: 375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq FLITLFCCCVVVG/FF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

Met Phe Phe Val His Phe Leu Ile Thr Leu Phe Cys Cys Cys Val Val
      -15                      -10                      -5

Val Gly Phe Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu
      1                      5                      10

Val Thr Trp Ala Arg Ala Gly
15                      20

```

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq CLLHLRCLQLYWA/AR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```

Met Ala Cys Phe Gly Glu Lys Arg His Ala Lys Ser Cys Leu Leu His
-25                      -20                      -15                      -10

Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala Arg
      -5                      1

```

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4  
seq PLSLALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Val Asp Arg Asp Glu Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro  
-25 -20 -15  
Leu Ser Leu Ala Leu Gln Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp  
-20 -15 -10 -5  
Cys Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly  
1 5 10

Gly

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ILLTSCFYTLVSS/TF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```

Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala Ser Leu
      -35                -30                -25

Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr Ser Cys
      -20                -15                -10

Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser Ser Leu
      -5                  1                  5

Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys Thr Phe
  10                  15                  20                  25

Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile Asn Phe
      30                35                40

Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu Phe Leu
      45                50                55

Ala Val Pro Arg
      60

```

## (2) INFORMATION FOR SEQ ID NO: 380:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq SFLCNFLVSLSL/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```

Met Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser
-20                -15                -10                -5

Leu Ser Leu Ser Phe Leu His Gly Arg

```

1

5

## (2) INFORMATION FOR SEQ ID NO: 381:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq LAYFLCCQGVIFG/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ala | Leu | Glu | Arg | Gly | Ser | Leu | Arg | Asn | Glu | Gln | Ala | Leu | Val |
|     |     |     | -30 |     |     |     |     | -25 |     |     |     |     | -20 |     |     |
| Ile | Tyr | Ala | Gly | Leu | Ala | Tyr | Phe | Leu | Cys | Cys | Gln | Gly | Val | Ile | Phe |
|     |     | -15 |     |     |     | -10 |     |     |     |     |     | -5  |     |     |     |
| Gly | Ser | Leu | Pro | Ser | Asn | Ala | Gly | Ala | Gly | Pro | Leu | Gly | Trp | Ser | Ser |
|     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq SLWFLPLPTHVYT/HT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Glu Tyr Leu Phe Gln Gln Pro Gly His Ser Arg Gly Glu Ala Arg  
                   -35                  -30                  -25

Ala Ala Ala Ala Ser Leu Glu Thr Leu Ser Ser Leu Trp Phe Leu Pro  
                   -20                  -15                  -10

Leu Pro Thr His Val Tyr Thr His Thr His Ala Asn  
                   -5                          1                  5

## (2) INFORMATION FOR SEQ ID NO: 383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq SSMLITILSFIFA/LG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Val Ser Ser Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu  
 -15                  -10                  -5                  1

Gly Tyr His Thr Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe  
                   5                  10                  15

Phe Leu His  
           20

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu Ala Ser Ser Ala  
-15 -10 -5

Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His Leu Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -39..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.2  
seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ile Cys Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu  
-35 -30 -25

Asn Arg Met Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu Leu His  
-20 -15 -10

Cys Ser Ile Arg Val Phe Phe Phe Phe  
-5 1

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq SFLLLQLIHEDKA/IQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Lys Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser  
-50 -45 -40

Phe Ser Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln  
-35 -30 -25

Val Pro Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile  
-20 -15 -10

His Glu Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu  
-5 1 5 10

Gln Leu

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq FGCTFVAFXPAFA/LS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Xaa Pro  
-15 -10 -5

Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg Gly  
1 5 10



## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LWSSCWLAFLADG/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg Arg Phe Gln Lys Gly  
                  -30                  -25                  -20

Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp Leu Ala Pro Leu Ala  
                  -15                  -10                  -5

Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln Arg Xaa Ala Ser Asn  
                  1                                  5                                  10

Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro Ala Pro Xaa Ala Ser  
15                                  20                                  25                                  30

Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro Trp Ala Ala Lys Met  
                                  35                                  40                                  45

Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala Gly Gly  
                  50                                  55

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ser Lys Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe  
-20 -15 -10

Tyr Gln Ile Ser Gly Arg Trp  
-5 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro Asp Ser Ala Gly  
-15 -10 -5 1

Pro Phe Leu Ser Pro Phe Ser  
5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq SFHFLPWALGAMA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```

Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys
      -30              -25              -20

Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala
      -15              -10              -5

Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg
      1              5              10

Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly
      15              20              25              30

Gly Gly Trp Met Gly Met Trp Val
      35

```

## (2) INFORMATION FOR SEQ ID NO: 392:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VIRLSQFLLKCWP/RT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```

Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
      -45              -40              -35

Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
      -30              -25              -20

Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
      -15              -10              -5              1

Thr Ser Leu Thr Ala Ala Thr

```

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq SFSIXTLLWGLNC/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe Lys Pro Leu Leu
-35                               -30                     -25

Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa Thr Leu Leu Trp
-20                               -15                     -10                     -5

Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu Arg Ile Val Xaa
      1                               5                     10

Ser Tyr Ser Ser Gly Tyr
      15

```

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq RLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val Gly Pro Gly  
 -40 -35 -30

Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg Leu Leu Leu  
 -25 -20 -15 -10

Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr Asp Val Asn  
 -5 1 5

Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg Ala Ser Leu  
 10 15 20

Gly

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys  
 -30 -25 -20

Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly  
 -15 -10 -5

Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys  
 1 5 10 15

His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro  
 20 25

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq AGLLP LLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu  
-20 -15 -10

Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys  
-5 1 5 10

Trp

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq TWLLLT LQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ile Leu Ser Thr Trp Leu Leu Leu Thr Leu Gln Asn Ser Val Phe  
-15 -10 -5

Thr Ser Phe Arg Ile Ser Pro Asn Arg Ile Gln Ser Met Leu Pro Pro  
1 5 10 15

Met

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq VCIVLALCHTSRP/MS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Phe His Ser Tyr Trp Gly Lys Ser Leu Gln Ser Phe Lys Thr  
-30 -25 -20

Phe Met Arg Val Cys Ile Val Leu Ala Leu Cys His Thr Ser Arg Pro  
-15 -10 -5

Met Ser Tyr His Val Pro Leu Ala Ala Gly Ser Pro Leu Met His Trp  
1 5 10 15

Ser Pro Cys Ser Pro Val Pro Phe Ile Gly  
20 25

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq RFTLLPLVLHSQS/SC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Lys Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser  
 -15 -10 -5

Ser Cys Val Phe Trp Lys Ala Gly  
 1 5

## (2) INFORMATION FOR SEQ ID NO: 400:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq FIPFLVIYSFVLS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg Phe  
 -30 -25 -20 -15

Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser Pro  
 -10 -5 1

His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu Cys  
 5 10 15

Asn Arg Ser  
 20

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:



(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -27..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.9  
 seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu  
 -25 -20 -15  
 Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg  
 -10 -5 1 5  
 Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys Thr Gly Val  
 10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -15..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.8  
 seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro Leu  
 -15 -10 -5 1  
 His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser Met  
 5 10 15  
 Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu  
 20 25

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -73..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

```

Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe Pro Leu Cys
    -70                      -65                      -60

Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro Leu Gln Arg
    -55                      -50                      -45

Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln Ala Arg Leu
    -40                      -35                      -30

Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val Ile Arg Ser
    -25                      -20                      -15                      -10

Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro Tyr Phe Ser
    -5                      1                      5

Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly Asn Ser Gly
    10                      15                      20

Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu Lys Met Xaa
    25                      30                      35

Val His
    40

```

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -14..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq SFIALVYSSLSFQ/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser Phe Gln Lys Val  
-10 -5 1  
Pro Gly

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Val Phe Asp Thr Leu Lys Ser Arg Ile Val Leu Phe Leu Asn Ser  
-20 -15 -10  
Xaa Phe Pro Ile Ile Cys Ser Arg  
-5 1

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -59..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq IFLFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu Cys Ser
      -55                -50                -45

Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu Leu Gly
      -40                -35                -30

Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys Ile Phe
      -25                -20                -15

Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys Asn Tyr
      -10                -5                1                5

Phe Arg Gly Asn Gly
              10
  
```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -17..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met Asp Asp Leu Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser
      -15                -10                -5

Gly Val Pro Ser Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala
      1                5                10                15

Glu Met Pro Pro Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu
              20                25                30

Pro Lys Pro Ala Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe
      35                40                45
  
```

Pro Val Gly Val Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly  
           50                          55                          60  
 Leu Gly His Ser Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val  
       65                          70                          75  
 Ser Pro Gly  
       80

## (2) INFORMATION FOR SEQ ID NO: 408:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LPTLLLLPVGAPG/KK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu Pro Thr Leu  
 -25                          -20                          -15                          -10  
 Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly Met Glu Gly  
                           -5                          1                          5  
 Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu Pro Gly Asp  
       10                          15                          20  
 His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr Arg Glu Gly  
       25                          30                          35  
 Ala Leu Thr Pro Pro Pro Gly  
       40                          45

## (2) INFORMATION FOR SEQ ID NO: 409:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq QTFVSFLSIPVLG/LV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met Leu Val Ser Lys Ile Gln Thr Phe Val Ser Phe Leu Ser Ile Pro
      -15                      -10                      -5

Val Leu Gly Leu Val Pro Asp His Ile Leu Gln Leu Ile Thr Glu Lys
      1                      5                      10

Glu Thr
      15

```

## (2) INFORMATION FOR SEQ ID NO: 410:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LLSTGLNILGTQA/FR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu His His
      -30                      -25                      -20

Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln Ala Phe
      -15                      -10                      -5                      1

Arg Tyr Glu Asp Gly Gln Leu
      5

```

## (2) INFORMATION FOR SEQ ID NO: 411:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq ILLWEACTGRCQA/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys Gln  
-15 -10 -5

Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu Val  
1 5 10 15

Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp Ala  
20 25 30

Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala Gly  
35 40 45

Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val Lys  
50 55 60

Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu  
65 70 75

## (2) INFORMATION FOR SEQ ID NO: 412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: . score 4.6  
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Thr Gly Tyr Pro Trp Ala Asn Ser Ile Thr Thr Val Leu Cys Ile  
-25                      -20                      -15                      -10  
Leu Gly Cys His Gly Asn Leu Cys Cys Glu Pro Ala Val Arg Ala Leu  
                    -5                      1                      5  
Gly

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IFTALFLXLHSVA/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu  
                    -20                      -15                      -10  
Phe Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe  
                    -5                      1                      5

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens



(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -20..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile Phe Leu Met Cys Leu  
 -20 -15 -10 -5

Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro  
 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -33..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
 seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Phe Gly Ala Gly Asp Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser  
 -30 -25 -20

Gly Gly Ala Arg Leu Ala Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa  
 -15 -10 -5

Gly His Gly Asn Glu Phe Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys  
 1 5 10 15

Lys Gly Gln Gly Thr Ala Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr  
 20 25 30

Ala Pro Ala Xaa Met Ser Thr Pro Thr Ile Leu Val Ala Thr Ala Val  
 35 40 45

His Ala Tyr Arg Tyr Thr Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu  
 50 55 60

Val Leu Gln Phe Trp  
65

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq RFLSLSAADGDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Thr | Leu | Gly | Glu | Ser | Trp | Pro | Val | Leu | Val | Gly | Arg | Arg |
|     |     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |
| Phe | Leu | Ser | Leu | Ser | Ala | Ala | Asp | Gly | Xaa | Asp | Xaa | Ser | Xaa | Asp | Ser |
|     | -10 |     |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |
| Trp | Asp | Val | Glu | Arg | Val | Ala | Glu | Trp | Pro | Trp | Leu | Ser | Gly | Thr | Ile |
| 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |
| Arg | Ala | Val | Ser | His | Thr | Asp | Val | Thr | Lys | Lys | Asp | Leu | Lys |     |     |
|     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln  
           -15                          -10                          -5  
 Gly Val Ser Asp Ser Ser Lys  
           1                                  5

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -50..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
                                   seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Glu Ser Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln  
 -50                          -45                          -40                          -35  
 Asn Gln Leu Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa  
                           -30                          -25                          -20  
 Xaa Xaa Ile Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr  
                           -15                          -10                          -5  
 Tyr Ala Ser Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile  
           1                                  5                                  10  
 Thr Glu Trp Leu  
 15

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids  
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4  
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly Val Leu Val Gly  
-25 -20 -15 -10

Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val Lys Gly Pro  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4  
seq GFLLCPLVCGGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe Leu Leu Cys Pro Leu  
-20 -15 -10

Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp Cys Cys Leu Ile Glu  
-5 1 5 10

Lys Thr His Arg Gly  
15

## (2) INFORMATION FOR SEQ ID NO: 421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq RGLLLGLAVAAAA/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Leu Arg Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala  
                  -15                                  -10                                          -5

Ala Ala Ala Val Arg  
                  1

## (2) INFORMATION FOR SEQ ID NO: 422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq ILLMIVFSIFLLL/CN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ile Leu Leu Met Ile Val Phe Ser Ile Phe Leu Leu Leu Cys Asn  
                  -10                                  -5                                          1

Leu Thr Asp Phe Tyr Leu Phe Arg Ser Asp Gly  
                  5                                  10

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION:  score 4.4
                        seq SLLFIFRSILISC/FS
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Ser Leu Leu Phe Ile Phe Arg Ser Ile Leu Ile Ser Cys Phe Ser  
-10 -5 1

Gly Asp Phe Phe Phe Phe  
5

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.3  
seq SKVLIQLSQAFWA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Pro Leu Ile Ser Lys Val Leu Ile Gln Leu Ser Gln Ala Phe Trp  
-15 -10 -5

Ala Ser Pro Glu Gly Arg Asn Ser Ser Gly Ser Lys Arg Lys Gln Leu  
 1 5 10 15

Val Ala Ala Val Glu Met Arg Tyr Cys Lys Arg Gln Gln Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro  
 -25 -20 -15

Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly  
 -10 -5 1

Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser Arg Ser Asn Lys  
 5 10 15

Phe Gln Asn Ser Ser Val Glu Asp Asp Asp Asp Val Val Phe Ile Glu  
 20 25 30 35

Pro Val Gln Pro Pro Pro Pro Ser Val Pro Val Val Ala Asp Gln Arg  
 40 45 50

Thr Ile Thr Phe Thr Ser Ser Lys Asn Xaa Glu Leu Gln Gly Asn Asp  
 55 60 65

Ser Lys Ile Thr Pro Ser Ser Lys Glu Leu Ala Ser  
 70 75

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3  
seq ILLLVTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

```
Met Asp Thr Gly Glu Ser Phe Ser Pro His Thr Ser Cys Arg Gly His
  -30                      -25                      -20

Trp Arg Ile Leu Leu Leu Thr His Val Pro Pro Trp Ile Leu Glu Asn
-15                      -10                      -5                      1

Pro Ser Cys His Thr Arg Pro Ala Val Asp Thr Gly Glu Ser Phe Ser
          5                      10                      15

Pro Gln Arg
      20
```

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3  
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

```
Met Pro Tyr Leu Asp Pro Tyr Ile Thr Gln Pro Ile Ile Gln Ile Glu
  -30                      -25                      -20

Arg Lys Leu Val Leu Leu Ser Val Leu Lys Glu Pro Val Ser Arg Ser
-15                      -10                      -5                      1
```



Ile Phe Asp Tyr Ala Leu Arg Ser Lys Asp Ile Thr Ser Leu Phe Arg  
                   5                  10                  15  
 His Leu His Met Arg Gln Lys Lys Arg Asn Gly Ser Leu Pro Asp Cys  
           20                  25                  30  
 Pro Pro Pro Glu Asp Pro Ala Ile Ala Gln Leu Leu Lys Lys Leu Leu  
       35                  40                  45  
 Ser Gln Gly Met Thr Glu Glu Glu Glu Asp Lys Leu Leu Ala Leu Lys  
   50                  55                  60                  65  
 Asp Phe Met Met

## (2) INFORMATION FOR SEQ ID NO: 428:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq VLLGSTAMATSLT/NV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro  
                   -25                  -20                  -15  
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly  
           -10                  -5                  1  
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser  
   5                  10                  15

## (2) INFORMATION FOR SEQ ID NO: 429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -28..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq FGLLDFVVQCCDS/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met His Val Leu Phe Asn Ile Val Thr Thr Asn Xaa Xaa Asn His Phe
      -25                      -20                      -15

Gly Leu Leu Asp Phe Val Val Gln Cys Cys Asp Ser Leu Arg Asn His
      -10                      -5                      1

Xaa Xaa Ser Phe Gln Ser Ser Tyr Leu Arg Leu Asn His Ser Xaa His
      5                      10                      15                      20

Thr Cys

```

## (2) INFORMATION FOR SEQ ID NO: 430:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -22..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq TAYWLSFMSWAQS/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```

Met Pro Pro Gln Ser Cys Cys Ser Lys Thr Ala Tyr Trp Leu Ser Phe
      -20                      -15                      -10

Met Ser Trp Ala Gln Ser Ser Ser Phe Gly Ser Arg Xaa Glu Ser Thr
      -5                      1                      5                      10

Ser Pro Cys Thr Asp His Cys Ser Gly Pro Arg Glu Glu Gln Leu Cys
      15                      20                      25

Ser Ser Arg Val Phe His Cys Ile Thr His Pro Asn Gly Arg Ile His

```

30

35

40

Arg Trp

## (2) INFORMATION FOR SEQ ID NO: 431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SCVFFHFLQGGLG/FG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Ser Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly  
                  -10                  -5                  1

Ser Ala Gly Arg Cys Ala Gly Asp Arg  
          5                  10

## (2) INFORMATION FOR SEQ ID NO: 432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq LILLPIWINMAQI/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Ser Ile Ser Leu Ser Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn  
 -20 -15 -10 -5

Met Ala Gln Ile Gln Gln Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr  
 1 5 10

Ala Leu Lys Asp Leu Leu Ser Arg Ile Asp Leu Asp Glu Leu Met Lys  
 15 20 25

Lys Asp Glu Pro Pro Gly  
 30

## (2) INFORMATION FOR SEQ ID NO: 433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SFCNAVVLSPVFQ/EE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Thr Ala Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly  
 -30 -25 -20

Ser Val Ser Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val  
 -15 -10 -5

Phe Gln Glu Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr  
 1 5 10

Trp Pro Pro Arg  
 15

## (2) INFORMATION FOR SEQ ID NO: 434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Trp Ser Arg Pro Val Gln Val Leu Gly Leu Leu Ala Thr Cys Gln  
-15 -10 -5  
His Ala Pro Ser Pro Ser Phe Lys Gly Glu Thr Cys Thr Glu Ile Glu  
1 5 10 15  
Ser Val Tyr Leu Ala Pro Met  
20

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln Ile  
-20 -15 -10  
Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser  
-5 1

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Pro Phe Phe Ser Asn Gln Pro Thr Gln Val Ser Val Leu Leu Phe  
-25 -20 -15 -10

Phe Cys Cys Ser Pro Leu Tyr Ser Pro Leu Phe Leu Leu Xaa Leu Ile  
-5 1 5

Pro His Gln  
10

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -44..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg  
-40 -35 -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile  
-25 -20 -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn  
-10 -5 1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu  
 5 10 15 20  
 Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser  
 25 30 35  
 Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn  
 40 45 50  
 Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu  
 55 60 65  
 Pro Leu Arg  
 70

## (2) INFORMATION FOR SEQ ID NO: 438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq GTYLTSSSPLCQL/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu Trp Leu  
 -40 -35 -30  
 Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His Thr Gly  
 -25 -20 -15  
 Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro Pro Gly  
 -10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq VLCCLLIATPTFF/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys Ile Gln  
-35 -30 -25 -20

Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala Thr Pro  
-15 -10 -5

Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg  
1 5

## (2) INFORMATION FOR SEQ ID NO: 440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq AGVVSTSVAAVA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser Val Ala Ala Ala  
-15 -10 -5

Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly  
1 5

## (2) INFORMATION FOR SEQ ID NO: 441:

## (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Trp Ile Met Ser Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile
-15                      -10                      -5                      1
Ser His Ser Leu Cys Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr Arg
-20                      -15                      -10                      -5
Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val Gln
      1                      5                      10
Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu Leu
      15                      20                      25

```

Pro Ser  
30

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met	Ile	Glu	Pro	Cys	Glu	Lys	Met	Lys	His	Tyr	Asp	Met	Asn	Trp	Phe	
				-40					-35						-30	
Leu	Cys	Met	Tyr	Glu	Cys	Phe	Phe	Phe	His	Leu	Leu	Glu	Thr	Glu	Phe	
			-25					-20						-15		
Leu	Leu	Pro	Cys	Val	His	Pro	Phe	Ser	Val	Ile	Ala	Val	Tyr	Val	Phe	
		-10					-5					1				

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq AALCGISLSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

```

Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro Gln Gln Pro Leu
-55                -50                -45                -40

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
                -35                -30                -25

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
                -20                -15                -10

Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
                -5                1

```

## (2) INFORMATION FOR SEQ ID NO: 445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq CLLVSYAVDSAAG/RF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

```

Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser Ala Ala
    -15                -10                -5

Gly Arg Phe Gly
    1

```

## (2) INFORMATION FOR SEQ ID NO: 446:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq ATLRCWASTPVSG/RL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```

Met Arg Lys Ile Ser His Cys Leu His Cys Trp Pro Glu Ser Gly Ala
      -25                      -20                      -15

Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser Gly Arg Leu Ser Ser
      -10                      -5                      1

Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro Gln Asp Ala Phe Thr
  5                      10                      15                      20

Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys Thr Glu Lys Glu Phe
      25                      30                      35

Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu Cys Glu Pro Gly Ala
      40                      45                      50

Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro Arg Glu Gly Leu Ser
      55                      60                      65

Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met Ser Leu Val Lys Lys
      70                      75                      80

Lys Gly Gln
      85

```

## (2) INFORMATION FOR SEQ ID NO: 447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LLHPCGSITLTSS/ST

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Cys Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser

```

-20

-15

-10

Ile Thr Leu Thr Ser Ser Ser Thr Thr Arg  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq VALQCGLTIPALX/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr Ile Pro Ala Leu  
 -15 -10 -5

Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln Asp Leu Arg Gly  
 1 5 10 15

Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro Ser  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -93..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9

seq LTSAFLWLPRHLI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Thr Val Arg Tyr Gly Lys Phe Leu Ser Leu Leu Lys Asp Gly Ala
    -90                      -85                      -80

Glu Asn Asp Leu Thr Trp Val Leu Lys His Cys Glu Arg Phe Leu Lys
    -75                      -70                      -65

Gln Gln Gln Thr Ser Ile Lys Ser Ser Leu Leu Cys Leu Gln Gly Asn
    -60                      -55                      -50

Tyr Ala Gly His Asp Trp Phe Val Ser Ser Leu Phe Met Ile Met Leu
    -45                      -40                      -35                      -30

Gly Asp Lys Glu Lys Thr Phe Gln Phe Leu His Gln Phe Ser Arg Leu
    -25                      -20                      -15

Leu Thr Ser Ala Phe Leu Trp Leu Pro Arg Leu His Ile Ser Val Arg
    -10                      -5                      1

Leu Gln Ser Val Phe Lys Gly Gly Phe Xaa Ile Leu Arg Thr Leu Tyr
    5                      10                      15

Leu His Ser Xaa Gly Arg
    20                      25

```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq FFWVVLFSAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
    -20                      -15                      -10                      -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu
    1                      5                      10

```

Ala Thr

## (2) INFORMATION FOR SEQ ID NO: 451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq HLSSTTSPPWTHA/AI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Leu Thr Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser  
-20 -15 -10

Pro Pro Trp Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu  
-5 1 5 10

Met Pro Ser Pro Arg Ile Trp Pro Leu  
15

## (2) INFORMATION FOR SEQ ID NO: 452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq CVNLLLGFEFVIS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

```

Met Arg Tyr Phe Gln Gly Pro Ser Pro Tyr Ser Glu Ile Glu Ile Glu
-40                               -35                               -30                               -25

Leu Cys Asp His Val Tyr Ser Phe Gln Gly Leu Cys Val Asn Leu Leu
                               -20                               -15                               -10

Leu Gly Phe Glu Pro Val Ile Ser Arg Ser Arg Xaa Ser Ser Leu Ala
                               -5                               1                               5

Val Glu Ser
    10

```

## (2) INFORMATION FOR SEQ ID NO: 453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq LASLECYVPSTNQ/WQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

```

Met Xaa Xaa Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu
-40                               -35                               -30

Val Tyr Ala Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu
-25                               -20                               -15                               -10

Glu Cys Tyr Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu
                               -5                               1                               5

Glu Val Ala Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val
    10                               15                               20

Leu Val Thr Gly Gly Leu
    25

```

## (2) INFORMATION FOR SEQ ID NO: 454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids



(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr Arg Asp  
-35 -30 -25  
Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His Leu Leu  
-20 -15 -10  
Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -27..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile  
-25 -20 -15  
Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu  
-10 -5 1 5  
Leu Leu Glu Leu

## (2) INFORMATION FOR SEQ ID NO: 456:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq RVAACTAAAPLQA/HG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala Ala Pro  
                  -15                  -10                  -5

Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa Leu Xaa  
                  1                  5                  10

Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu His Gln  
          15                  20                  25

Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala  
          30                  35                  40

## (2) INFORMATION FOR SEQ ID NO: 457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RWASSCLHPSARS/SN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

```

Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro Arg Pro Ala Leu Pro
      -30                -25                -20

Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys Leu His Pro Ser Ala
      -15                -10                -5

Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg Thr Pro
      1                5                10

```

## (2) INFORMATION FOR SEQ ID NO: 458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LCPVIFFPSNCWK/EY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

```

Met Gln Gly Val Arg Gly Pro Val Ser Phe Ser Trp Ser Thr Thr Met
      -25                -20                -15

Leu Cys Pro Val Ile Phe Phe Pro Ser Asn Cys Trp Lys Glu Tyr Asn
      -10                -5                1

Arg Thr Gln
      5

```

## (2) INFORMATION FOR SEQ ID NO: 459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq FXLLFXXFXFFRQ/XG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe  
          -15                          -10                          -5

Arg Gln Xaa Gly  
                  1

## (2) INFORMATION FOR SEQ ID NO: 460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq SVRLLFRRFSVIMA/SE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe  
          -20                          -15                          -10

Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile  
          -5                          1                          5

## (2) INFORMATION FOR SEQ ID NO: 461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala Phe Pro Leu Leu Ser  
-15 -10 -5  
Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -37..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Glu Glu Glu Ala Ala Gln Ile Pro Arg Ser Ser Val Trp Glu  
-35 -30 -25  
Gln Asp Gln Gln Asn Val Val Gln Arg Val Val Ala Leu Pro Leu Val  
-20 -15 -10  
Arg Ala Thr Cys Thr Ala Val Cys Asp Val Tyr Ser Ala Ala Lys Asp  
-5 1 5 10  
Arg His Pro Leu Leu Gly Ser Ala Trp  
15 20

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly Pro  
-70 -65 -60

Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly Ile  
-55 -50 -45

Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile Lys  
-40 -35 -30 -25

Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu Thr  
-20 -15 -10

Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val Ile  
-5 1 5

Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys Phe  
10 15 20

Arg  
25

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -117..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8

seq XXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr
  -115                      -110                      -105

Pro Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser
  -100                      -95                      -90

Glu Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu
  -85                      -80                      -75                      -70

Arg Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val
                      -65                      -60                      -55

Cys Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His
                      -50                      -45                      -40

Leu Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu
  -35                      -30                      -25

Cys Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys
  -20                      -15                      -10

Pro Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser
  -5                      1                      5                      10

Thr Leu

```

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7

seq MIEMILIFLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

```

Met Ile Glu Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp
  -10                      -5                      1

```

Thr Ile Thr Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu  
           5                          10                          15  
 Gln Phe Tyr Leu Pro Ser Phe Leu Leu Leu Glu  
      20                          25                          30

## (2) INFORMATION FOR SEQ ID NO: 466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq VIGSLLVLTMLTC/RR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met His Pro Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr  
                           -75                          -70                          -65  
 Lys His Ser Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His  
                           -60                          -55                          -50  
 Ile Leu Gly Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr  
                           -45                          -40                          -35  
 Lys Cys Leu Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile  
                           -30                          -25                          -20  
 Ala Ile Val Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg  
                           -15                          -10                          -5                          1  
 Arg

## (2) INFORMATION FOR SEQ ID NO: 467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:



(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -14..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```
Met Ile Trp Pro Met Ser Ala Ser Val Ala Thr Leu Trp Ser Phe Thr
      -10                      -5                      1
Ser Tyr Ile Ser Tyr Pro Ser Arg Phe Tyr Tyr Asp Ala Trp
      5                      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 468:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -31..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp Phe His Pro
  -30                      -25                      -20
Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu Leu Cys Thr
-15                      -10                      -5                      1
Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn Ala Gln Ile
      5                      10                      15
Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys Pro Phe Lys
      20                      25                      30
Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu Arg Ile Glu
      35                      40                      45
Cys Gln Gly Asn Gly
```

50

## (2) INFORMATION FOR SEQ ID NO: 469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -87..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LILQASLKGELEA/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Lys Glu Leu Asn Gln Lys Leu Thr Asn Lys Asn Asn Lys Ile Glu
      -85                      -80                      -75

Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys Gln Lys Gln Glu Thr Leu
      -70                      -65                      -60

Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser Val Gln Glu Tyr Glu Glu
-55                      -50                      -45                      -40

Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val Lys Thr Lys Lys Glu Leu
      -35                      -30                      -25

Ala Asp Ser Lys Gln Ala Glu Thr Asp His Leu Ile Leu Gln Ala Ser
      -20                      -15                      -10

Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln Gln Val Glu Val Tyr Lys
      -5                      1                      5

Val Arg Val Leu Leu Phe Lys Ile Lys Lys Met Phe Phe His Val Glu
      10                      15                      20                      25

Val Arg Asn Gly

```

## (2) INFORMATION FOR SEQ ID NO: 470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq RLLLCILIIVCYI/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Asn Thr Leu Lys Glu Met Gln Asp Val Gln Gly Ala Leu Gln
      -110                      -105                      -100

Cys Tyr Thr Arg Ala Ile Gln Ile Asn Pro Ala Phe Ala Asp Ala His
      -95                      -90                      -85

Ser Asn Leu Ala Ser Ile His Lys Asp Ser Gly Asn Ile Pro Glu Ala
      -80                      -75                      -70

Ile Ala Ser Tyr Arg Thr Ala Leu Lys Leu Lys Pro Asp Phe Pro Asp
      -65                      -60                      -55                      -50

Ala Tyr Cys Asn Leu Ala His Cys Leu Gln Ile Val Cys Asp Trp Thr
      -45                      -40                      -35

Asp Tyr Asp Glu Arg Met Lys Lys Leu Val Ser Ile Val Ala Asp Gln
      -30                      -25                      -20

Leu Glu Lys Asn Arg Leu Leu Leu Cys Ile Leu Ile Ile Val Cys Tyr
      -15                      -10                      -5

Ile Leu Phe Leu Met
      1

```

## (2) INFORMATION FOR SEQ ID NO: 471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq VAYAIPSPISLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

```

Met Leu Ile Leu Ala Asp Thr Arg Arg Val Gln Gly Gly Thr Leu Gly
      -35                      -30                      -25

Leu Ile Pro Ala Val Leu Asn Arg Val His Val Ala Tyr Ala Ile Pro
      -20                      -15                      -10

Ser Ile Pro Ser Leu Phe Cys Gln Arg Trp
      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

```

Met Leu Val Gly Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser
-20                      -15                      -10                      -5

Asn Thr Ser Ser Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile
      1                      5                      10

Pro Pro His Gly
      15

```

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser  
-40 -35 -30  
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu  
-25 -20 -15  
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys  
-10 -5 1 5  
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr  
10 15 20  
Ser Leu Gly  
25

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val  
-15 -10 -5  
Ser Gly Ile Pro Gly Leu Leu Thr  
1 5

## (2) INFORMATION FOR SEQ ID NO: 475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq RWLCLQAYLASFS/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val  
-45 -40 -35

Gly Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser  
-30 -25 -20 -15

Gln Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu  
-10 -5 1

Ser Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro  
5 10 15

Pro Pro  
20

## (2) INFORMATION FOR SEQ ID NO: 476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu
  -20                      -15                      -10

Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu
  -5                      1                      5                      10

Leu Arg Thr Val Lys Met Met Arg Val Met
          15                      20

```

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq CFWGLMYXWLLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Asn Gly Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly
-35                      -30                      -25                      -20

Asp Leu Arg Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu
          -15                      -10                      -5

Leu Leu Gly Ser Xaa Gly
          1

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.7  
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser  
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg  
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser  
15 20 25

Ser Arg His Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro  
30 35 40

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala  
45 50 55

Xaa Thr Ile Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr  
60 65 70 75

Leu

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LMLLVSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser  
-20 -15 -10



Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg  
       -5                                  1                                  5                                  10  
 Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile  
                                   15                                  20                                  25  
 Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu  
                                   30                                  35                                  40  
 Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Leu Lys  
                                   45                                  50                                  55  
 His Arg  
       60

## (2) INFORMATION FOR SEQ ID NO: 480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq VLELLAAVCLVRG/GH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser His Pro His Ala  
       -45                                  -40                                  -35  
 Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn Pro Arg Thr Lys  
       -30                                  -25                                  -20  
 Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu Val Arg Gly Gly  
       -15                                  -10                                  -5                                  1  
 His Glu Ile Ile Leu Ser Ala Phe Asp Asn Phe Lys Glu Val Cys Gly  
                                   5                                  10                                  15  
 Glu Lys Gln Arg Phe Glu Lys Leu Met Glu His Phe Arg Asn Glu Asp  
                                   20                                  25                                  30  
 Asn Asn Ile Asp Phe Met Val Ala Ser Met Gln Phe Ile Asn Ile Val  
       35                                  40                                  45  
 Val His Ser Val Glu Asp Met Asn Phe Arg Val His Leu Gln Tyr Glu  
       50                                  55                                  60                                  65

Phe Thr Lys Leu Gly Leu Xaa Glu Tyr Leu Xaa Lys Leu Lys His Thr  
                     70                    75                    80

Glu Ser Asp Lys Leu Gln Val Gln Ile  
                     85                    90

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7  
seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp Gly Leu  
                     -25                    -20                    -15

Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu Phe Arg  
                     -10                    -5                    1

His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn Phe Leu  
                     5                    10                    15                    20

Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln  
                     25                    30

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.1  
seq LHLFHLIRPXOG/WX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met	Gly	Ser	Gly	Tyr	Ser	His	Ser	Leu	His	Leu	Phe	His	Leu	Leu	Ile
-20						-15					-10				
Arg	Pro	Xaa	Gln	Gly	Trp	Xaa	Xaa	Ile	Val	Pro	Ala	Cys	Phe	Trp	Arg
-5					1				5					10	
Lys	Lys	Ile	Leu	Thr	Pro	Ser	Thr	Gly	Thr	Met	Glu	Leu	Leu	Gln	Val
			15					20					25		
Thr	Ile	Leu	Phe	Leu	Leu	Pro	Ser	Ile	Cys	Ser	Ser	Asn	Ser	Thr	Gly
		30					35					40			
Val	Leu	Glu	Ala	Ala	Asn	Asn	Ser	Leu	Val	Val	Thr	Thr	Thr	Lys	Pro
	45					50					55				
Ser	Ile	Thr	Thr	Pro	Asn	Thr	Trp								
60						65									

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr  
-15 -10 -5

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
1 5 10 15

Gln Val Ser Cys Arg Ile Met Xaa Xaa Thr Leu Val Ser Lys Lys Ala  
20 25 30

Asn Gln Gln Leu Asn Phe Thr Glu Xaa Xaa Gly Gly Xaa Xaa Ala Ala  
35 40 45  
Gly Thr Lys Phe Gly  
50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq MTCLSVLFGYATS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu  
-30 -25 -20  
Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr  
-15 -10 -5  
Ser His Pro Gln Gly Leu Tyr Ile  
1 5

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3  
seq RQLLLPLPPFSFP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

```
Met Pro Gln Gln Pro Val Glu Gln Gly Ser Pro Leu Leu Arg Gln Leu
-25 -20 -15

Leu Leu Pro Leu Pro Pro Phe Ser Phe Pro Ala Pro Ser Pro Cys Pro
-10 -5 1 5

Ser Trp Pro Val Ala Leu Gly Ser His Gly Val Ala Tyr Trp Gly Ser
10 15 20

Cys Ser Leu Gly His
25
```

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -80..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 6.2
                               seq RASLLPMLLGSWA/FL
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met	Pro	Ser	Arg	Ser	Pro	Phe	Thr	Trp	Ser	His	Leu	Cys	Trp	Arg	Ala
-80					-75					-70					-65
Gly	Arg	Cys	Pro	Arg	Trp	Arg	Ala	Cys	Leu	Ser	Ser	Ser	Ser	Val	Arg
				-60					-55					-50	
Met	Cys	Ser	Pro	Ala	Ala	Pro	Ser	Arg	Phe	Gly	Ala	Leu	Gly	Xaa	Ser
			-45					-40					-35		
Ala	Arg	Arg	Trp	Pro	Arg	Arg	Asp	Ala	Asp	Thr	Trp	Cys	Ala	Pro	Gln
		-30					-25					-20			
Gly	Val	Met	Arg	Ala	Ser	Leu	Leu	Pro	Met	Leu	Leu	Gly	Ser	Trp	Ala
	-15					-10					-5				
Phe	Leu	Pro	Pro	Ser	Cys	Ser	Pro	Arg	Ala						
1				5					10						

## (2) INFORMATION FOR SEQ ID NO: 487:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LTYGIILTHGASG/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Met Ser His Thr Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu  
-40                      -35                      -30                      -25

Leu Asp Ala Val Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile  
                    -20                      -15                      -10

Ile Leu Thr His Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met  
                    -5                      1                      5

Ser Leu Ala Ser His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe  
                    10                      15                      20

Thr Cys Lys Gly Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser  
                    25                      30                      35                      40

Val Leu Asn Tyr Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly  
                    45                      50                      55

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LCXEFXSVASCD/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40                -35                -30                -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Xaa Glu Phe
                -20                -15                -10

Xaa Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
                -5                1                5

Xaa Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
    10                15                20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Xaa
    25                30                35

```

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Gly Arg Thr Tyr Ile Val Glu Glu Thr Val Gly Gln Tyr Leu Ser
-35                -30                -25

Asn Ile Asn Leu Gln Gly Lys Ala Phe Val Ser Gly Leu Leu Ile Gly
-20                -15                -10                -5

Gln Cys Ser Ser Gln Lys Asp Tyr Val Ile Leu Ala Thr Arg Thr Pro
                1                5                10

Pro Lys Glu Glu Gln Ser Glu Asn Leu
    15                20

```

## (2) INFORMATION FOR SEQ ID NO: 490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                      -15                      -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                      1                      5                      10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                      20                      25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                      35                      40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                      50                      55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                      65                      70                      75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                      85                      90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg
95                      100

```

## (2) INFORMATION FOR SEQ ID NO: 491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20              -15              -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5              1              5              10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15              20              25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30              35              40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45              50              55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60              65              70              75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80              85              90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly Trp Glu
95              100             105

Tyr Ala Phe Glu Gly Thr Xaa Gly Arg Phe Leu Thr Asp Ser Ser Ile
110             115             120

Trp Ile Gln Cys Leu Glu
125

```

## (2) INFORMATION FOR SEQ ID NO: 492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq SFLPSALVIWTS/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
  -20                      -15                      -10

Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
  -5                      1                      5                      10

Leu His His Ile
                15

```

## (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq PLIFSLWCSGVLL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```

Met Phe Asn Ala Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe
  -40                      -35                      -30

Val Phe Thr Phe Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe
  -25                      -20                      -15                      -10

Ser Leu Trp Cys Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly
                -5                      1                      5

Gly Pro Arg Leu Trp Arg Ile His Gly Glu Gln
  10                      15

```

## (2) INFORMATION FOR SEQ ID NO: 494:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -29..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 13.4  
                            seq SLLLVLQLLTPCSA/QF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val  
                  -25                  -20                  -15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser  
                  -10                  -5                          1

Val Leu Gly Pro Leu  
                  5

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 47 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -42..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.2  
                            seq LLFDLVCHEFCQS/DD
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala  
          -40                  -35                          -30

Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe  
 -25 -20 -15

Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Arg  
 -10 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq PMQLLQVLSDVLA/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro  
 -40 -35 -30

Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met  
 -25 -20 -15

Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys  
 -10 -5 1 5

Gln Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg  
 10 15 20

Met Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala  
 25 30 35

Thr Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro  
 40 45 50

Val Ile Tyr Pro Val Leu  
 55

## (2) INFORMATION FOR SEQ ID NO: 497:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq IIHAXGLVRECLA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
Met Ala Thr Ser Ser Gln Xaa Arg Gln Leu Leu Ser Asp Tyr Gly Pro
               -75                      -70                      -65

Pro Ser Leu Gly Tyr Thr Gln Gly Thr Gly Asn Ser Gln Xaa Pro Gln
               -60                      -55                      -50

Ser Lys Tyr Ala Glu Leu Leu Ala Ile Ile Xaa Glu Leu Gly Lys Glu
               -45                      -40                      -35

Ile Arg Pro Met Tyr Ala Gly Ser Lys Ser Ala Met Glu Arg Leu Lys
               -30                      -25                      -20

Arg Gly Ile Ile His Ala Xaa Gly Leu Val Arg Glu Cys Leu Ala Xaa
-15                      -10                      -5                      1

Thr Glu Arg Met Pro Asp Pro Ser Cys Leu Val Gly Phe
      5                      10
```

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```

Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
-15          -10          -5          1
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
          5          10          15
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
          20          25          30
Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys
          35          40

```

## (2) INFORMATION FOR SEQ ID NO: 499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq RLLRRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

```

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser
-15          -10          -5
Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
1          5          10          15
Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro
          20          25          30
Ala Pro Gly
          35

```

## (2) INFORMATION FOR SEQ ID NO: 500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq LNSLSALAEAVG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15                      -10                      -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1              5              10              15

```

## (2) INFORMATION FOR SEQ ID NO: 501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq YTAVSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

```

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60                      -55                      -50

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45                      -40                      -35                      -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
-25                      -20                      -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
-10                      -5                      1

Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5              10              15

```

Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Thr Thr Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser  
-15 -10 -5

Arg Ser Ser Phe Gln  
1 5

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14.1  
seq LTLLLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:



Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu Thr Leu Leu  
 -25 -20 -15 -10

Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu Leu Ala  
 -5 1 5

Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn Val Thr Val  
 10 15 20

Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly Arg Leu Phe  
 25 30 35

Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile Ala Val Tyr  
 40 45 50 55

Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys Ala Val  
 60 65 70

Gly Ser Ile Leu Ser Glu Gly Glu  
 75

## (2) INFORMATION FOR SEQ ID NO: 504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4  
seq LWSLALWLPLALS/VS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Gly Thr Glu Met Gly Ala Arg Pro Gly Gly His Pro Xaa Lys  
 -30 -25 -20

Trp Ser Phe Leu Trp Ser Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser  
 -15 -10 -5

Val Ser Leu Phe Leu Gly Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu  
 1 5 10 15

Ser Leu Trp Cys Thr Leu Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys  
 20 25 30

Gly Thr Pro Ser Pro Ala Leu Leu Asn Leu Gly Thr Arg Gly  
 35 40 45

## (2) INFORMATION FOR SEQ ID NO: 505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq LLFALGSLGLIFA/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu Ser Leu Gln Val Leu  
-55 -50 -45 -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg  
-35 -30 -25

Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly  
-20 -15 -10

Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn Xaa His Lys Tyr Pro  
-5 1 5

Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Xaa Ala Leu Thr  
10 15 20 25

Val Ala Val Val Val Thr  
30

## (2) INFORMATION FOR SEQ ID NO: 506:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: -38..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.8  
 seq MLLLLLLLGSGQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg  
                   -35                                  -30                                  -25  
 Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu Leu  
                   -20                                  -15                                  -10  
 Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly  
           -5  1  5

(2) INFORMATION FOR SEQ ID NO: 507:

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 53 amino acids  
     (B) TYPE: AMINO ACID  
     (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
     (A) ORGANISM: Homo Sapiens  
     (D) DEVELOPMENTAL STAGE: Fetal  
     (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
     (A) NAME/KEY: sig\_peptide  
     (B) LOCATION: -41..-1  
     (C) IDENTIFICATION METHOD: Von Heijne matrix  
     (D) OTHER INFORMATION: score 9.9  
                                   seq ILPFLLFPFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val Thr Ser Asn Thr  
       -40                                  -35                                  -30  
 Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln Ile Leu Pro Phe  
       -25                                  -20                                  -15                                  -10  
 Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His Xaa Val Ala Gln  
                   -5  1  5  
 Thr Lys Ser Pro Arg  
                   10

(2) INFORMATION FOR SEQ ID NO: 508:

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 38 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.7  
seq QLCLLLLPCSLVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Pro Gly Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro  
-20 -15 -10

Ser Cys Ser Leu Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe  
-5 1 5 10

Ser Thr Thr Ser Arg Glu  
15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -93..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.6  
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Arg His Gly Phe Ile Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser  
-90 -85 -80

Xaa Xaa Xaa Xaa Ile Phe Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser  
-75 -70 -65

Ser Ala Ala Pro Lys His Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu

-60                      -55                      -50  
 Gln Gly Gln Gln Leu Asn Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser  
 -45                      -40                      -35                      -30  
 Cys Val Leu Ala Ser Ser Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly  
                     -25                      -20                      -15  
 Leu Ser Leu Ser Leu Gly Ala Ser Ala Pro Val Gln Cys Gln Gln Asp  
                     -10                      -5                      1  
 Asn Tyr Thr Phe Cys Xaa Gln Tyr Trp Leu Arg Ala Arg His  
       5                      10                      15

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LIIFLSFLPFINS/SF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val Pro Phe Val Arg Gly  
       -40                      -35                      -30  
 Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val Ile Leu Ile Ile Phe  
 -25                      -20                      -15                      -10  
 Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe Val Tyr Lys Thr Asn  
                     -5                      1                      5  
 Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe Ser Phe Arg Tyr Pro  
       10                      15                      20  
 Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu Val Phe  
       25                      30                      35

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq FPVLALFLSGSLA/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Ser Leu Ser Gln Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser  
-20 -15 -10 -5  
Gly Ser Leu Ala Leu Phe His His Thr Ser Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -29..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val  
-25 -20 -15  
Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys  
-10 -5 1  
Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr  
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu  
20 25 30 35

Val Lys Xaa Pro Pro Arg  
40

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
-30 -25 -20

Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly  
-15 -10 -5

Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

seq LLVLLLYAPVGFC/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -90..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.4  
seq SLVLLTVTPSXRO/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Ala Gln Ser Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys  
-90 -85 -80 -75

Lys Gly Phe Phe Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg  
-70 -65 -60

Val Ala Cys Val Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu  
-55 -50 -45



Asn Pro Gly Gly Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp  
 -40 -35 -30

Lys Val Arg Asn Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val  
 -25 -20 -15

Leu Leu Thr Val Thr Pro Ser Xaa Arg Gln Gln Glu  
 -10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 516:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq WLLVLSFVFGCNV/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser  
 -20 -15 -10

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa Xaa Xaa  
 -5 1 5

Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu Ser Gln  
 10 15 20 25

Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn  
 30 35 40

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys Ile Asn  
 45 50 55

Lys Met Thr Asp Lys  
 60

## (2) INFORMATION FOR SEQ ID NO: 517:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq HVFFLLLLAHIIA/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Asn Leu Phe Lys Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala  
-20 -15 -10 -5

His Ile Ile Ala Leu Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe  
1 5 10

Gly Asn

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg  
-20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro  
-5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly  
10 15

## (2) INFORMATION FOR SEQ ID NO: 519:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser  
-65 -60 -55  
Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr  
-50 -45 -40 -35  
Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro  
-30 -25 -20  
Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala  
-15 -10 -5  
Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser  
1 5 10  
Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg  
15 20 25 30

## (2) INFORMATION FOR SEQ ID NO: 520:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

```

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
      -20                      -15                      -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
      -5                      1                      5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
      10                      15                      20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
      25                      30                      35                      40

Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile Pro Gln Ile
      45                      50                      55

Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp Ser Glu Val
      60                      65                      70

Leu Met Met Ile Lys Thr Gln Ala
      75                      80

```

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -92...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

```

Met Glu Ala Ser Trp Gly Ser Phe Asn Ala Glu Arg Gly Trp Tyr Val
      -90                      -85                      -80

Ser Val Gln Gln Pro Glu Glu Ala Glu Ala Glu Glu Leu Ser Pro Leu
      -75                      -70                      -65

```

Leu Ser Asn Glu Leu His Arg Gln Arg Ser Pro Gly Val Ser Phe Gly  
 -60 -55 -50 -45  
 Leu Ser Val Phe Asn Leu Met Asn Ala Ile Met Gly Ser Gly Ile Leu  
 -40 -35 -30  
 Gly Leu Ala Tyr Val Met Ala Asn Thr Gly Val Phe Gly Phe Ser Phe  
 -25 -20 -15  
 Leu Leu Leu Thr Val Ala Leu Leu Ala Ser Tyr Ser Val His Leu Leu  
 -10 -5 1  
 Leu Ser Met Cys Ile Gln Thr Ala Val Thr Ser Tyr Glu Asp Leu Gly  
 5 10 15 20  
 Leu Phe Ala Phe Gly Leu Pro Gly Leu  
 25

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FFLLLRFFLRIDG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp  
 -15 -10 -5  
 Gly Val Pro  
 1

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser  
                  -15                  -10                  -5  
Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp  
                  1                          5                  10  
Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu  
          15                          20                  25

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq VLLLAALPPVLLP/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala  
                  -20                  -15                  -10  
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu  
                  -5                          1                  5  
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe  
          10                          15                  20                  25  
Tyr Gln Pro Met Pro Leu Xaa Ala Ser Leu Glu Ile Glu  
                  30                          35

## (2) INFORMATION FOR SEQ ID NO: 525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq LLSACLVTWGLG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His  
-35 -30 -25

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr  
-20 -15 -10

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val  
-5 1 5 10

Leu Xaa Leu Ala Ser Leu Gln Leu Gly  
15 20

## (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq HLLLLLLPAPTLK/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His  
                   -25                  -20                  -15

His Leu Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly  
                   -10                  -5                  1

Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu  
           5                  10                  15

Thr Leu Leu Gln Ser Gly  
   20                  25

## (2) INFORMATION FOR SEQ ID NO: 527:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LLFIIGLIGCCAT/IR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu  
   -75                  -70                  -65                  -60

Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala  
                   -55                  -50                  -45

Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val  
                   -40                  -35                  -30

Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu  
                   -25                  -20                  -15

Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg  
                   -10                  -5                  1                  5

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr  
                   10                  15                  20

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu  
                   25                  30                  35

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys  
                   40                  45



## (2) INFORMATION FOR SEQ ID NO: 528:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq IGHFLCLVILVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```

Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65                               -55                               -50
Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
-45                               -40                               -35
Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
-30                               -25                               -20
Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
-15                               -10                               -5
Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
1                               5                               10                               15
Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
20                               25                               30
Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
35                               40                               45
Val Trp Lys
50

```

## (2) INFORMATION FOR SEQ ID NO: 529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -14..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
 seq LLLSLFFPLRISL/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile Ser Leu Ser Pro  
                   -10                  -5                  1  
 Ser Asn His Leu Trp Ser Ala Ser Ser Gly  
                   5                  10

## (2) INFORMATION FOR SEQ ID NO: 530:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -23..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.6  
 seq LILVLQLLLRIRR/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Glu Thr Gly Glu Arg Ala Arg Leu Ile Leu Ile Leu Val Leu Gln  
                   -20                  -15                  -10  
 Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln Gln Arg Cys Xaa Ala Ser  
                   -5                  1                  5  
 Ser Ala Thr Ala Pro Ser Ser His Gly Cys Asp Leu Arg Gly Gly Lys  
   10                  15                  20                  25  
 Leu Asn Phe Lys Thr Thr Pro Met Asp Ala Asp Ser Asp Val Ala Leu  
                   30                  35                  40  
 Asp Ile Leu Ile Thr Asn Val Val Cys Val Phe Arg Thr Arg Cys Arg

45

50

55

## (2) INFORMATION FOR SEQ ID NO: 531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq ILGCSSVCQLCTG/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe Leu Val  
-40 -35 -30

Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Glu Ile Leu Gly Cys  
-25 -20 -15 -10

Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys Arg Asn  
-5 1 5

Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln Phe Phe  
10 15 20

Cys Ile  
25

## (2) INFORMATION FOR SEQ ID NO: 532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -73..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq ACCFLSAFSPTLT/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro Pro Ser  
-70 -65 -60  
Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys Asp Gln  
-55 -50 -45  
Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro Arg Leu  
-40 -35 -30  
Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys Cys Phe  
-25 -20 -15 -10  
Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala Thr Ser  
-5 1 5  
Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe Thr Lys  
10 15 20  
Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys Lys Gln  
25 30 35  
Glu Lys Ser Thr Thr Pro Gln  
40 45

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr  
-20 -15 -10  
Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp

-5

1

5

## (2) INFORMATION FOR SEQ ID NO: 534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq GVGLVTLLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly  
-25 -20 -15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg  
-10 -5 1 5

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Ser Glu Lys Tyr Leu  
10 15 20

Leu Arg Leu Leu Asp Lys Thr Thr Pro Gly  
25 30

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq VLLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Tyr Pro Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe
  -50                      -45                      -40

Leu Lys Gln Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu
-35                      -30                      -25                      -20

Ala Leu Arg Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val
                      -15                      -10                      -5

Xaa Xaa Ser Ser Pro Leu Glu Phe Ile Arg
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq ILLXTFQTWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu Lys Leu Xaa Thr
      -30                      -25                      -20

Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln Thr Trp Cys Leu
      -15                      -10                      -5

Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg Xaa Gly Cys Leu
      1                      5                      10                      15

Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq TLKFLTLQKSNA/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

```
Met Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr
      -20                -15                -10

Leu Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His
      -5                1                5

Asp Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu
  10                15                20                25

Cys Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile
                30                35                40

Tyr Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn
      45                50                55

Ala Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn
      60                65                70

Phe Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr
      75                80                85

Ile Phe Glu
  90
```

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9

seq ALALAXAPDLAQA/PL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu
    -25                      -20                      -15

Ala Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro
    -10                      -5                      1                      5

Gly Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn
                      10                      15                      20

Gly Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr
                      25                      30                      35

Asn Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly
    40                      45                      50

Gly Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His
    55                      60                      65

Pro Val Arg Leu Phe Trp
    70                      75

```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7

seq ILGLLGLLGLTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
    -20                      -15                      -10

Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
    -5                      1                      5

Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys

```



10                      15                      20  
 Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln Cys  
 25                      30                      35                      40  
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala  
                     45                      50                      55  
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile  
                     60                      65                      70  
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg  
                     75                      80                      85  
 Ala Arg  
                     90

## (2) INFORMATION FOR SEQ ID NO: 540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ILGLLGLLGTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu  
                     -20                      -15                      -10  
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr  
                     -5                      1                      5  
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys  
                     10                      15                      20  
 Gly Leu Trp Met Glu Cys Ala  
                     25                      30

## (2) INFORMATION FOR SEQ ID NO: 541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Val Ala Gly  
-15 -10 -5

Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr  
1 5 10

Asp Ala Ala Ser Gly Thr Met Arg Lys Ser  
15 20

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq LWYVCPCPSGAWM/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Ser Arg Leu Cys Gly Gly Ala Leu Trp Tyr Val Cys Pro Cys  
-20 -15 -10

Pro Ser Gly Ala Trp Met Val Pro Gly  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LGYLVLSEGAFLA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu  
-25 -20 -15  
Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp  
-10 -5 1  
Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu Val Ser  
5 10 15 20  
Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Arg  
25 30 35

## (2) INFORMATION FOR SEQ ID NO: 544:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
    -40                      -35                      -30

Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa Ile Xaa Trp Ile Thr Gly
    -25                      -20                      -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
    -10                      -5                      1                      5

Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Xaa Leu
        10                      15                      20

Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu Gly Tyr Arg
        25                      30                      35

```

## (2) INFORMATION FOR SEQ ID NO: 545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq VLLGSGLTILSQP/LM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

```

Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
    -20                      -15                      -10                      -5

Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
        1                      5                      10

Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
        15                      20                      25

Xaa Xaa Leu Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
        30                      35                      40

```

## (2) INFORMATION FOR SEQ ID NO: 546:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser  
-20 -15 -10 -5  
Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro His Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LWCFHLVVLISLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Pro His Gly Leu Trp Cys Phe His Leu Val Val Leu Ser Leu Tyr  
-15 -10 -5  
Ser Ser Val Ala Thr Ala Arg  
1 5

(2) INFORMATION FOR SEQ ID NO: 548:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -14..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5  
                                seq SLVAVFLSCGLIS/KN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly Leu Ile Ser Lys Asn  
                    -10                    -5                    1

His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile Pro His Asn Ala Asn  
            5                    10                    15

His Leu Leu  
    20

(2) INFORMATION FOR SEQ ID NO: 549:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 42 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -24..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5  
                                seq GALAVGAVPVVLS/AM
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Met Lys Arg Ala Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val  
            -20                    -15                    -10

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly  
            -5                    1                    5

Ile Ala Ala Ser Ser Ile Ala Ala His Gly  
 10 15

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met	Ala	Val	Ile	Val	Asp	Lys	Pro	Trp	Phe	Tyr	Asp	Met	Lys	Lys	Val	-30	-75	-70
Trp	Glu	Gly	Tyr	Pro	Ile	Gln	Ser	Thr	Ile	Pro	Ser	Gln	Tyr	Trp	Tyr	-65	-60	-55
Tyr	Met	Ile	Glu	Leu	Ser	Phe	Tyr	Trp	Ser	Leu	Leu	Phe	Ser	Ile	Ala	-45	-40	-35
Ser	Asp	Val	Lys	Arg	Lys	Asp	Phe	Lys	Glu	Gln	Ile	Ile	His	His	Val	-30	-25	-20
Ala	Thr	Ile	Ile	Leu	Ile	Ser	Phe	Ser	Trp	Phe	Ala	Asn	Tyr	Ile	Arg	-15	-10	-5
Ala	Gly	Thr	Leu	Ile	Met	Ala	Leu	His	Asp	Ser	Ser	Asp	Tyr	Leu	Leu	1	5	10
Glu	Ser	Ala	Lys	Met	Phe	Asn	Tyr	Ala	Gly	Trp	Lys	Asn	Thr	Cys	Asn	20	25	30
Asn	Ile	Phe	Thr	Val	Phe	Ala	Ile	Val	Phe	Ile	Ile	Thr	Arg	Leu	Val	35	40	45
Ile	Leu	Pro	Phe	Trp	Ile	Leu	His	Cys								50	55	

(2) INFORMATION FOR SEQ ID NO: 551:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLFIYIFLTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr  
-15 -10 -5

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala  
1 5 10 15

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe  
20 25 30

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile  
35 40 45

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Gly Thr  
50 55 60

## (2) INFORMATION FOR SEQ ID NO: 552:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq LQMLLG FVGRSKS/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:



```

Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg
  -30                -25                -20
Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
  -15                -10                -5
Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe
  1                5                10                15
Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr
      20                25                30
Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro
      35                40                45
Leu Asp Pro Leu Thr Gly
      50

```

## (2) INFORMATION FOR SEQ ID NO: 553:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VHALCPLSPLVTT/GC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```

Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp Val
-60                -55                -50                -45
Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro Glu
      -40                -35                -30
Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln Val
      -25                -20                -15
His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys Gly
      -10                -5                1
Gln Ala Ala
      5

```

## (2) INFORMATION FOR SEQ ID NO: 554:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq GLLGXGLXXXSLT/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu Thr Ile  
-30 -25 -20

Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu Thr Ala  
-15 -10 -5 1

Gly

## (2) INFORMATION FOR SEQ ID NO: 555:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LIVWLLVKSFSES/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu

-50                      -45                      -40  
 Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro  
                          -35                      -30                      -25  
 Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val  
                          -20                      -15                      -10  
 Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp  
                          -5                      1                      5                      10  
 Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys  
                          15                      20                      25  
 Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu  
                          30                      35                      40  
 Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys His Ala Gln Glu Thr  
                          45                      50                      55  
 Thr Ser Leu Leu Trp Xaa Leu Ile Ser His  
                          60                      65

## (2) INFORMATION FOR SEQ ID NO: 556:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LLDSSLMASGTAS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Asp Lys Asp Ser Gln Gly Leu Leu Asp Ser Ser Leu Met Ala Ser  
 -20                      -15                      -10                      -5  
 Gly Thr Ala Ser Arg Ser Glu Asp Glu Glu Ser Leu Ala Gly Gln Lys  
                          1                      5                      10  
 Arg Ala Ser Ser Gln Ala Leu Gly Thr Gly  
                          15                      20

## (2) INFORMATION FOR SEQ ID NO: 557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq CLAVSWEAAGCHG/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Gly Leu Leu Thr Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu  
-35 -30 -25

His Asn Pro Asp His His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala  
-20 -15 -10 -5

Gly Cys His Gly Ala Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly  
1 5 10

Pro Trp Arg Pro Arg Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg  
15 20 25

Ser Leu His Lys Gln Val Ile Leu Phe Gly Leu Leu Gly Phe Ala Tyr  
30 35 40

Asp His Trp  
45

## (2) INFORMATION FOR SEQ ID NO: 558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

```

Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly Val Glu Ser
  -15                -10                -5

Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln Leu Pro Glu
  1                5                10                15

Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala Leu Leu Arg
      20                25                30

Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln Cys Glu Glu
      35                40                45

Ala

```

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

```

Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
  -60                -55                -50

Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
  -45                -40                -35

Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
  -30                -25                -20                -15

Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
      -10                -5                1

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
      5                10                15

Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Arg
      20                25                30

```

## (2) INFORMATION FOR SEQ ID NO: 560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq WLLRLAYLADIFT/KL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

```

Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg Trp
          -60                      -55                      -50

Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg Glu
          -45                      -40                      -35

Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu Thr
          -30                      -25                      -20

Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe Thr
          -15                      -10                      -5

Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr Val
  1              5              10              15

Phe Thr Val Phe Asp Lys Met Ser Ser Leu Leu Arg Lys Leu Glu Phe
          20              25              30

Trp Ala Ser Ser Val Glu Glu Glu Asn Phe Asp Cys Phe Pro Thr Leu
          35              40              45

Ser Asp Phe Leu Thr Glu Ile Asn Ser Thr Val Asp Lys Asp Ile Cys
          50              55              60

Ser Ala Ile Val Gln His Leu Arg Gly Leu Arg Ala Thr Leu Leu Lys
          65              70              75              80

Tyr Phe Pro Val Thr Asn Asp
          85

```

## (2) INFORMATION FOR SEQ ID NO: 561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

```
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25                -20                -15                -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5                1                5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
      10                15
```

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

```
Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp Val Leu Ala His
-50                -45                -40

Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu Ile Gly Glu Phe
-35                -30                -25                -20

Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu Val Leu Gly Cys
```

Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln Arg Ile Met Thr  
1 5 10  
Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala Ile Gln Glu Leu  
15 20 25  
Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu Thr Tyr Gly Asn  
30 35 40 45  
Phe Asp Ser Gln Ser Arg Ser Thr Gly  
50

## (2) INFORMATION FOR SEQ ID NO: 563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MIHGFCLAPTTS/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala  
-10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide



(B) LOCATION: -17..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: . score 3.7  
 seq RTWCLACVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Xaa Cys Pro Arg Thr Trp Cys Leu Ala Cys Val Glu Ala Ser Pro  
 -15 -10 -5

Gly Gln Pro Phe Leu Pro Pro Arg Pro Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His  
 -20 -15 -10

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  
 -5 1 5 10

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp  
 15 20 25

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Xaa Arg Cys  
 30 35 40

Gln Ala Gly  
 45

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids  
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Phe Lys Val Ala Ala Pro Pro Met Leu Ile Xaa Xaa Ile Ile Met  
-25 -20 -15

Phe Leu Leu Ile Ile Val Cys Gly Ser Pro Arg Pro  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXMCLWSLRNLFS/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser Leu  
-20 -15 -10

Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser Leu  
-5 1 5 10

His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn Asn  
15 20 25

Gly Ser Ala  
30

## (2) INFORMATION FOR SEQ ID NO: 568:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq SVPLLSLSHSIGI/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Ser Pro Ala Gly Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe  
                  -30                  -25                  -20  
Val Ala Leu Asp Gly Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile  
                  -15                  -10                  -5  
Gly Ile Ser Pro Thr Arg  
                  1

## (2) INFORMATION FOR SEQ ID NO: 569:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LVCVGLHTEGPWG/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met His Trp Ala Leu Val Cys Val Gly Leu His Thr Glu Gly Pro Trp  
           -15                          -10                          -5

Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser Gly Met Asp Arg Ala Arg  
       1                              5                          10                          15

Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala Ser Gln Thr Pro Gln  
                           20                          25                          30

## (2) INFORMATION FOR SEQ ID NO: 570:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu Val Leu Leu Glu Lys  
           -70                          -65                          -60

Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu Asp Arg Glu Arg Met  
       -55                          -50                          -45

His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu Leu Asn Phe Met Ile  
       -40                          -35                          -30                          -25

Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp Phe Tyr Ile Gly  
                           -20                          -15                          -10

Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro Ala His Phe  
           -5                          1                          5

## (2) INFORMATION FOR SEQ ID NO: 571:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart .

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -27..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq VVALLIVCDVPSA/SA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

```

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
  -25                      -20                      -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Arg
  -10                      -5                      1

```

## (2) INFORMATION FOR SEQ ID NO: 572:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LLLQPSMIQEVWT/XY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

```

Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp Thr
  -15                      -10                      -5

Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe Gln
  1                      5                      10                      15

Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met Gln
  20                      25                      30

Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His Asp
  35                      40                      45

```

## (2) INFORMATION FOR SEQ ID NO: 573:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LAVLLSLAPSASS/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Leu His Leu His Xaa Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro  
-30 -25 -20

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp  
-15 -10 -5 1

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu  
5 10 15

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro  
20 25 30

Xaa Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile  
35 40 45

Ser Ala Ala Ser Leu Cys  
50 55

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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup>:</b> <b>C12N 15/12, C07K 14/47</b>	<b>A2</b>	<b>(11) International Publication Number:</b> <b>WO 99/06554</b> <b>(43) International Publication Date:</b> 11 February 1999 (11.02.99)
<b>(21) International Application Number:</b> PCT/IB98/01238 <b>(22) International Filing Date:</b> 31 July 1998 (31.07.98) <b>(30) Priority Data:</b> 08/905,134      1 August 1997 (01.08.97)      US <b>(71) Applicant (for all designated States except US):</b> GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). <b>(74) Agents:</b> MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>

**(54) Title:** 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES

**(57) Abstract**

The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.





## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/12, C07K 14/47</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 99/06554</b> <b>(43) International Publication Date:</b> 11 February 1999 (11.02.99)
<b>(21) International Application Number:</b> PCT/IB98/01238 <b>(22) International Filing Date:</b> 31 July 1998 (31.07.98) <b>(30) Priority Data:</b> 08/905,134                      1 August 1997 (01.08.97)                      US <b>(71) Applicant (for all designated States except US):</b> GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). <b>(74) Agents:</b> MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>  <b>(88) Date of publication of the international search report:</b> 27 May 1999 (27.05.99)
<b>(54) Title:</b> 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES  <b>(57) Abstract</b>  The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.		

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# INTERNATIONAL SEARCH REPORT

In International Application No

PCT/IB 98/01238

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12N C07K

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

### C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 98 44114 A (INCYTE PHARMACEUTICALS INC. (US); HILLMAN JENNIFER L.; GOLI SURYA K.) 8 October 1998 see abstract see page 12, line 5-14 see page 42 - page 43 see page 46 - page 47; claims --- -/--	1-11, 15-37

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

<sup>o</sup> Special categories of cited documents :

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
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10 November 1998

Date of mailing of the international search report

010399

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01238

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	<p>WO 98 42738 A (HUMAN GENOME SCIENCES INC. (US); YOUNG PAUL ET AL.) 1 October 1998  see page 40, line 34 - page 41, line 35  Gene No.46  see page 79  see page 100, line 23-25  Seq.ID:56  see page 209 - page 210  Seq.ID:110  see page 259 - page 260  Seq.ID:170  see page 297 - page 298  Seq.ID:224  see page 331 - page 332  see page 381 - page 384; claims</p>	1-28, 34-37
X	<p>Database EMBL Emest7, Entry HS1150166  Accession number AA232452  6 March 1997  96% identity with Seq.ID:38 nt.41-140  XP002083765</p>	1-11, 15-37
Y	<p>see the whole document</p>	12-14
Y	<p>YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator"  GENE,  vol. 163, 1995, pages 193-196, XP002053953  see abstract</p>	12,13
Y	<p>LIN Y. ET AL.: "Inhibition of nuclear translocation of transcription factor NF-kB by a synthetic peptide containing a cell membrane-permeable motif and nuclear localization sequence"  JOURNAL OF BIOLOGICAL CHEMISTRY,  vol. 270, no. 24, 16 June 1995, pages 14255-14258, XP002050723  cited in the application  see abstract</p>	14
A	<p>OZAWA M.: "Cloning of a human homologue of mouse reticulocalbin reveals conservation of structural domains in the novel endoplasmic reticulum resident Ca<sup>2+</sup>-binding protein with multiple EF-hand motifs"  JOURNAL OF BIOCHEMISTRY,  vol. 117, 1995, pages 1113-1119, XP002070128</p>	

-/--

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01238

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SCHÄFER B.W. AND HEIZMANN C.W.: "The S100 family of EF-hand calcium-binding proteins: functions and pathology" TIBS TRENDS IN BIOCHEMICAL SCIENCES, vol. 21, no. 4, April 1996, page 134-140 XP004050923 ---	
A	WO 96 34981 A (GENSET (FR); MERENKOVA IRENA NICOLAEVNA; DUMAS MILNE EDWARDS JEAN) 7 November 1996 cited in the application ---	
A	KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application ---	
A	EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 cited in the application ---	
A	CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996, pages 327-336, XP002081729 cited in the application ---	
A	WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 ---	
A	TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993, pages 600-603, XP000673204 ---	
A	HEIJNE VON G.: "A new method for predicting signal sequence cleavage sites" NUCLEIC ACIDS RESEARCH, vol. 14, no. 11, 1986, pages 4683-4690, XP002053954 cited in the application -----	

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/IB 98/01238

## Box I Observations where certain claims were found uns archabl (C ntinuation of it m 1 of first sh et)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

See extra sheet, Invention 1.

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:306, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

Inventions 2-268: Claims 1-37 all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-305, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 307, invention 3 is limited to Seq.ID:40 and 308,....., invention 147 is limited to Seq.ID:305 and 573).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

## INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 98/01238

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9844114	A	08-10-1998	AU 6787598 A	22-10-1998
WO 9842738	A	01-10-1998	AU 6564698 A	12-10-1998
			AU 6562798 A	20-10-1998
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			AU 5982996 A	21-11-1996
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			WO 9408001 A	14-04-1994
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WO 9707198	A	27-02-1997	US 5707829 A	13-01-1998
			AU 6712396 A	18-02-1997
			AU 6768596 A	12-03-1997
			CA 2227220 A	06-02-1997
			CA 2229208 A	27-02-1997
			EP 0839196 A	06-05-1998
			EP 0851875 A	08-07-1998
			WO 9704097 A	06-02-1997